

SEARCH REQUEST FORM

Scientific and Technical Information Center

Access DB# 52181

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher _____	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone # _____	AA Sequence (#) <u>4</u>	Dialog _____
Searcher Location _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up <u>10/31/01</u>	Bibliographic _____	Dr Link _____
Date Completed <u>10/5/01</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time _____	Fulltext _____	Sequence Systems <u>04</u>
Clerical Prep Time _____	Patent Family _____	WWW/Internet _____
Online Time _____	Other _____	Other (specify) _____

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Db 601 GTCACGATAG 612

RESULT 3
US-08-770-379-17/c
Sequence 17, Application US/08770379
Patent No. 5849564
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-17

Query Match 100.0%; Score 612; DB 2; Length 35100;
Best Local Similarity 100.0%; Pred. No. 2.5e-200;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTGCTGTTCAAGTGTGCTCTCTCTGTCGTTCACTGTCGTATCTGGAACG 60
Db 17875 ATGTGCTGTTCAAGTGTGCTCTCTCTGTCGTTCACTGTCGTATCTGGAACG 17816
QY 61 CGGGGCAAGTGGCCGAGCCGCCGAGTTGAAAAAGATCTTTCATTCAGAGACTCAAT 120
Db 17815 CGGGGCAAGTGGCCGAGCCGCCGAGTTGAAAAAGATCTTTCATTCAGAGACTCAAT 17756
QY 121 TGGATGCTATGAGGTCGATGATGATGCTCCGCACTCTGTACCGGATCCGATCTGC 180
Db 17755 TGGATGCTATGAGGTCGATGATGATGCTCCGCACTCTGTACCGGATCCGATCTGC 17696
QY 181 AAGGATCTAGAGCCCGCTGCTATTTTCATCTGAAACTACAGCAGCATCAAGATACT 240
Db 17695 AAGGATCTAGAGCCCGCTGCTATTTTCATCTGAAACTACAGCAGCATCAAGATACT 17636
QY 241 GATCACTGCGGGTTAATAGATTTAATGAGACTGCTGCTTAAAAAGCTGCCGATGCC 300
Db 17635 GATCACTGCGGGTTAATAGATTTAATGAGACTGCTGCTTAAAAAGCTGCCGATGCC 17576

QY 301 TTTTGAATTCGAGGCTGTTTAACTTTTAACGACGAGTGTGAAAAATCAGTGATA 360
Db 17575 TTTTGAATTCGAGGCTGTTTAACTTTTAACGACGAGTGTGAAAAATCAGTGATA 17516
QY 361 AACGTGACGTCATGAGGCTTCTGACGACGCTTGTAGATGGACATACGAAAGAGCTC 420
Db 17515 AACGTGACGTCATGAGGCTTCTGACGACGCTTGTAGATGGACATACGAAAGAGCTC 17456
QY 421 AATAGCTGACTAAGACGACACTACAGTCCACCCAAATTTGACCGGCTATTAGGAGG 480
Db 17455 AATAGCTGACTAAGACGACACTACAGTCCACCCAAATTTGACCGGCTATTAGGAGG 17396
QY 481 CTCGAGGACTTAAGTATTTGGGGGAGACACTTTCCTGTTTATGTTTCAGTGCATG 540
Db 17395 CTCGAGGACTTAAGTATTTGGGGGAGACACTTTCCTGTTTATGTTTCAGTGCATG 17336
QY 541 GAAAAGTTGACGTCAGGAGGCTGCTTTTGGACTCTATCCAGACGAGCTCCGAC 600
Db 17335 GAAAAGTTGACGTCAGGAGGCTGCTTTTGGACTCTATCCAGACGAGCTCCGAC 17276
QY 601 GTCACGATAG 612
Db 17275 GTCACGATAG 17264

RESULT 4
US-08-757-669A-17/c
Sequence 17, Application US/08757669A
Patent No. 6183751
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,669A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 45185-F
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 35100 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-757-669A-17
Query Match 100.0%; Score 612; DB 4; Length 35100;

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RESULT 2
US-08-686-349-1
Sequence 1, Application US/08686349
Patent No. 5861500
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: KAPOSI'S SARCOMA-ASSOCIATED HERPES VIRUS (KSHV)
TITLE OF INVENTION: INTERLEUKIN 6 (IL-6) AND USES THEREOF
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

QY	1	ATGTGCTGGTCAAGTTGGAGTCTCTTGGTGGCGTTCACCTGGTGAATCTGAAGC	6
Dp	1	ATGAGCTGGTCAAGTTGGAGTCTCTTGGTGGCGTTCACCTGGTGAATCTGAAGC	60
QY	61	CGGCGCAAGTTGCCGAGCGCCCGCAGTTTGGAAAAAGATCTTCTACATTCAGAGACTCAAT	120
Dp	61	CGGCGCAAGTTGCCGAGCGCCCGCAGTTTGGAAAAAGATCTTCTACATTCAGAGACTCAAT	120
QY	121	TGGATGCTAATGGGTATTCGATGAAATGCTTCGCGACCTCTGTTACCGTACCGGCAATTCGC	180
Dp	121	TGGATGCTAATGGGTATTCGATGAAATGCTTCGCGACCTCTGTTACCGTACCGGCAATTCGC	180
QY	181	AAGGATATTCAGAGCGCGCGTCTATTTTCATGTGAAATACACAGCATCAACGATCT	240
Dp	181	AAGGATATTCAGAGCGCGCGTCTATTTTCATGTGAAATACACAGCATCAACGATCT	240
QY	241	GATCACTCGCGGGTAAATAGATTTAATGACACTAGCTGCCTTAAAAAGCTCGCGGATGGC	300
Dp	241	GATCACTCGCGGGTAAATAGATTTAATGACACTAGCTGCCTTAAAAAGCTCGCGGATGGC	300
QY	301	TTTTTGAATTTGAGGTGTGTTTAAAGTTTAAACAGCGAGTTTGGAAAAATCAAGTATA	360
Dp	301	TTTTTGAATTTGAGGTGTGTTTAAAGTTTAAACAGCGAGTTTGGAAAAATCAAGTATA	360
QY	361	AACGTGAGCATGTGAGACTTCTGACGAAACCTTAAGATGGGACATACAGGAAGAGCTC	420
Dp	361	AACGTGAGCATGTGAGACTTCTGACGAAACCTTAAGATGGGACATACAGGAAGAGCTC	420
QY	421	AATAAGCTACTAAGACGCACTACAGTCCACCCAAATTTGGACCGCGGTATTAGGAGAG	480
Dp	421	AATAAGCTACTAAGACGCACTACAGTCCACCCAAATTTGGACCGCGGTATTAGGAGAG	480
QY	481	CTTCAGGAGCTTAAGTATTGGGTGAGACACTTTCGTTTATGTCTGAGTGCATATG	540
Dp	481	CTTCAGGAGCTTAAGTATTGGGTGAGACACTTTCGTTTATGTCTGAGTGCATATG	540
QY	541	GAAATGTTGACAGTCAAGCGGTGGGTTTGGACCTATCCCAAGCTGACTCTCAG	600
Dp	541	GAAATGTTGACAGTCAAGCGGTGGGTTTGGACCTATCCCAAGCTGACTCTCAG	600
QY	601	GTCACAGATAG	612

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:51:09 ; Search time 32.27 Seconds
(without alignments)
130.165 Million cell updates/sec

Title: US-09-230-048-2
Perfect score: 1095

Sequence: 1 MCFKMLVSLVSGT.....GQAVRLDIPDVPVHDK 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	992	90.6	185	US-09-122-443-16	Sequence 16, App1
2	183.5	16.8	184	US-08-945-529-12	Sequence 12, App1
3	183	16.7	185	US-07-918-181A-4	Sequence 4, App1
4	183	16.7	185	US-07-918-181A-8	Sequence 8, App1
5	183	16.7	185	US-08-231-575-4	Sequence 4, App1
6	183	16.7	185	US-08-231-575-8	Sequence 8, App1
7	183	16.7	185	PCT-US93-06928-4	Sequence 4, App1
8	183	16.7	185	PCT-US93-06928-8	Sequence 8, App1
9	183	16.7	212	US-08-792-019B-9	Sequence 9, App1
10	183	16.7	212	US-08-988-819-9	Sequence 9, App1
11	183	16.7	212	US-09-016-534-9	Sequence 9, App1
12	183	16.7	212	US-08-097-869-7	Sequence 7, App1
13	183	16.7	212	US-08-795-473B-6	Sequence 6, App1
14	183	16.7	212	5510472-2	Patent No. 5510472
15	182	16.6	184	US-08-693-182-2	Sequence 2, App1
16	182	16.6	184	US-09-008-482-2	Sequence 2, App1
17	181	16.5	183	US-08-009-973-1	Sequence 1, App1
18	181	16.5	184	US-08-567-047-2	Sequence 2, App1
19	181	16.5	184	US-08-567-048-2	Sequence 2, App1
20	181	16.5	184	5186931-1	Patent No. 5186931
21	181	16.5	185	US-07-632-070B-1	Sequence 1, App1
22	181	16.5	185	US-07-918-181A-2	Sequence 2, App1
23	181	16.5	185	US-07-918-181A-6	Sequence 6, App1
24	181	16.5	185	US-08-231-575-2	Sequence 2, App1
25	181	16.5	185	US-08-231-575-6	Sequence 6, App1
26	181	16.5	185	US-08-246-427A-5	Sequence 5, App1
27	181	16.5	185	US-08-716-317-7	Sequence 7, App1

28	181	16.5	185	US-08-766-620-5	Sequence 5, App1
29	181	16.5	185	PCT-US93-06928-2	Sequence 2, App1
30	181	16.5	185	PCT-US93-06928-6	Sequence 6, App1
31	181	16.5	185	5186931-2	Patent No. 5186931
32	181	16.5	186	US-07-632-070B-2	Sequence 2, App1
33	181	16.5	186	US-07-745-382-20	Sequence 20, App1
34	181	16.5	186	US-07-921-848-20	Sequence 20, App1
35	181	16.5	186	US-08-165-301A-20	Sequence 20, App1
36	181	16.5	186	US-08-469-318-163	Sequence 163, App
37	181	16.5	186	US-08-468-609A-163	Sequence 163, App
38	181	16.5	186	US-08-810-436-20	Sequence 20, App1
39	181	16.5	186	PCT-US94-14179-20	Sequence 20, App1
40	181	16.5	186	PCT-US95-01185-163	Sequence 163, App
41	181	16.5	187	US-07-632-070B-3	Sequence 3, App1
42	181	16.5	188	US-09-122-443-12	Sequence 12, App1
43	181	16.5	317	US-08-469-318-145	Sequence 145, App
44	181	16.5	317	US-08-468-609A-145	Sequence 145, App
45	181	16.5	317	PCT-US95-01185-145	Sequence 145, App

ALIGNMENTS

RESULT 1
US-09-122-443-16
Sequence 16, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ. ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-16

Query Match 90.6%; Score 992; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 3.2e+11;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
20 TRKLPDAPFEKDLIORLNMMLWVDECFRDLCTRTGICKILEPAATFHLKLPAIND 79
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Db 1 TRGKLPDAPPEKDLIQRNMMMLVIDECFRDLCYRTGCKGILEPAIFHLKLPAIND 60
QY 80 TDHCGI,GFNETSCLKLIADGFEFEVLKFLTTEFGKSVINVDVMEI,LTTLGMDIOEE 139
Db 61 TDHCGI,GFNETSCLKLIADGFEFEVLKFLTTEFGKSVINVDVMEI,LTTLGMDIOEE 120
QY 140 LNKLTHTYSPKEDRGLGLGRLGKLVVRIIPASFYVLSAMEKFAQAVRLDSTPDVTP 199
Db 121 LNKLTHTYSPKEDRGLGLGRLGKLVVRIIPASFYVLSAMEKFAQAVRLDSTPDVTP 180
QY 200 DVHDK 204
Db 181 DVHDK 185

RESULT 2
US-08-945-529-12
Sequence 12, Application US/08945529
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: PAONESSA, Giacomo
TITLE OF INVENTION: ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT
TITLE OF INVENTION: ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROMIDY AND NEIMARK, P. L. L. C.
STREET: 419 Seventh Street N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/945,529
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM95A000273
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT96/00084
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: CILIBERTO-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: pepptide
US-08-945-529-12

Query Match 16.8%; Score 183.5; DB 2; Length 184;
Best Local Similarity 27.4%; Pred. No. 3.3e-14;
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1;
QY 46 IDFCFRDLCYRTGCKGILEPAIFHLKLPAINDTHGCLIGFNETSCL 94
Db 25 IDKQIRLDIFISALRKETCKSNKCSSKEDAFWNLNPKMAEKDGCFFKGFNETCL 84

QY 95 KKLADGFEFEVLKFLTTEFGKSVINVDVMEI,LTTLGMDIOEE,LNKLTHTYSPKED 154
Db 85 VKIITGLLEFEVLEYLVQNNRESSEQARAQVOMRKD,LIQRLQKAKKALDATTPTTN 144
QY 155 RGLGRLOGLKLVVRIIPASFYVLSAMEKFAQAVRL 191
Db 145 ASLTLKLOAQONQWLODMTHLILRSFKFELIRLSRAL 181

RESULT 3
US-07-918-181A-4
Sequence 4, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 mutants
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-918-181A-4

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
QY 28 PEFEKDLIQRNMMMLVIDECFRDLCYRTGCKGILEPAIFHLKLPAINDTHGCLIG 87
Db 19 PLTSSERIDKQIRYLDISALRKETCKSNKCSSKEDALFNNLNP,PKMAEKDGCFFOSC 78
QY 88 FNETSCLKLIADGFEFEVLKFLTTEFGKSVINVDVMEI,LTTLGMDIOEE,LNKLTHTY 147
Db 79 FNETCLVKIITGLLEFEVLEYLVQNNRESSEQARAQVOMRKD,LIQRLQKAKKALDATTPTTN 138
QY 148 YSPKEDRGLGLGRLGKLVVRIIPASFYVLSAMEKFAQAVRL 191
Db 139 TPDPPTNASLTLKLOAQONQWLODMTHLILRSFKFELIRLSRAL 182

RESULT 4
US-07-918-181A-8
Sequence 8, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.


```

: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/918,181A
: FILING DATE: 23-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: POW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-07-918-181A-8

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Query Match          16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

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QY 28 PEFEKDLIORLNMMLWIDECFRLCYRTGICGILEPAIFHLKLPAINDTDHCGLIG 87
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Db 19 PLTSSERIDKQIRYLIDGISALRKETCNKSMCKSSKEALANNLNPKMAEKGCRCOSG 78

QY 88 FNETSCLKLADGFEFEVLEFKFLITEFGKSVINVDWELLTKTLGMDIOEELNKLKRTTH 147
   ||| : ||| : | |||| : : | : : : : : | : : : : : |
Db 79 FNETCLVKKITGILEFEVYLEYLQNRFESSEEQARAVQMSKTVLIQFLQKKANLDAIT 138

QY 148 YSPPKPDRGLGRLOGLKYWRHFSFYLSAMKFPAGQAVRL 191
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Db 139 TPDPPTNASTLTKLQAOQNWLDQMTHTLLKSLKEFMOSLRAL 182

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RESULT 5
US-08-231-575-4
: Sequence 4, Application US/08231575
: Patent No. 5565336
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/231,575

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: FILING DATE: 22-APR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/918,181
: FILING DATE: 23-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: POW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-231-575-4

```

```

Query Match          16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

```

```

QY 28 PEFEKDLIORLNMMLWIDECFRLCYRTGICGILEPAIFHLKLPAINDTDHCGLIG 87
   | : : : : : | : : : : : | : : : : : | : : : : : |
Db 19 PLTSSERIDKQIRYLIDGISALRKETCNKSMCKSSKEALANNLNPKMAEKGCRCOSG 78

QY 88 FNETSCLKLADGFEFEVLEFKFLITEFGKSVINVDWELLTKTLGMDIOEELNKLKRTTH 147
   ||| : ||| : | |||| : : | : : : : : | : : : : : |
Db 79 FNETCLVKKITGILEFEVYLEYLQNRFESSEEQARAVQMSKTVLIQFLQKKANLDAIT 138

QY 148 YSPPKPDRGLGRLOGLKYWRHFSFYLSAMKFPAGQAVRL 191
   | : : : : : | : : : : : | : : : : : | : : : : : |
Db 139 TPDPPTNASTLTKLQAOQNWLDQMTHTLLKSLKEFMOSLRAL 182

```

```

RESULT 6
US-08-231-575-8
: Sequence 8, Application US/08231575
: Patent No. 5565336
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated
: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/231,575
: FILING DATE: 22-APR-1994
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/918,181
: FILING DATE: 23-JUL-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: POW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 8:

```

SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-231-575-8

Query Match 16.7%; Score 183; DB 1; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;

QY 28 PEFKDLQRLNMMWVDECFRDICYRTGICKGLEPAALFHLPAINDTHGGLIG 87
DB 19 PLTSSRIDKQIRYILDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCGCFOSG 78
QY 88 FNETSCLAKLADGFFFEVLFKFLTTEFGKSVINVDWMLLTGMDIOEELNKLTKTH 147
DB 79 FNETCLVAKIITGLLEFEVLEYLQNRFFESSEQARAQVMSKVLQFQKKAKNLDALT 138
QY 148 YSPPKFDRGLGRLOGIKYWRHFASFVYLSAMEKFAQAVRVL 191
DB 139 TPDPPTNASLITKIQANQWMDMTHTLILRSLEKFMQSSLRAL 182

RESULT 7
PCT-US93-06928-4
Sequence 4, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOM-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06928-4

Query Match 16.7%; Score 183; DB 5; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
QY 28 PEFKDLQRLNMMWVDECFRDICYRTGICKGLEPAALFHLPAINDTHGGLIG 87
DB 19 PLTSSRIDKQIRYILDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCGCFOSG 78

DB 19 PLTSSRIDKQIRYILDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCGCFOSG 78
QY 88 FNETSCLAKLADGFFFEVLFKFLTTEFGKSVINVDWMLLTGMDIOEELNKLTKTH 147
DB 79 FNETCLVAKIITGLLEFEVLEYLQNRFFESSEQARAQVMSKVLQFQKKAKNLDALT 138
QY 148 YSPPKFDRGLGRLOGIKYWRHFASFVYLSAMEKFAQAVRVL 191
DB 139 TPDPPTNASLITKIQANQWMDMTHTLILRSLEKFMQSSLRAL 182

RESULT 8
PCT-US93-06928-8
Sequence 8, Application PC/TUS9306928
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESS: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOM-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06928-8

Query Match 16.7%; Score 183; DB 5; Length 185;
Best Local Similarity 25.6%; Pred. No. 3.9e-14;
Matches 42; Conservative 38; Mismatches 84; Indels 0; Gaps 0;
QY 28 PEFKDLQRLNMMWVDECFRDICYRTGICKGLEPAALFHLPAINDTHGGLIG 87
DB 19 PLTSSRIDKQIRYILDGISALRKETCNKSNMCESSKEALAEENNLLPKMAEKDCGCFOSG 78
QY 88 FNETSCLAKLADGFFFEVLFKFLTTEFGKSVINVDWMLLTGMDIOEELNKLTKTH 147
DB 79 FNETCLVAKIITGLLEFEVLEYLQNRFFESSEQARAQVMSKVLQFQKKAKNLDALT 138
QY 148 YSPPKFDRGLGRLOGIKYWRHFASFVYLSAMEKFAQAVRVL 191
DB 139 TPDPPTNASLITKIQANQWMDMTHTLILRSLEKFMQSSLRAL 182
RESULT 9
US-08-792-019B-9
Sequence 9, Application US/08792019B

```
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9
```

```
Query Match 16.7%; Score 183; DB 1; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRINMLMNVIDECFRLCYRT 57
DB 16 LGILLVLPAPAPVPPGEDSKDVAAPHROPJTSSERIDQIRYILDGISALRKETCKMS 75
QY 58 GICGKILEPAIFHLKLPAINDTDHGCLIGFNETSCLKLADGFEEFEVLEKFLTFEFGK 117
DB 76 NMCESSKEALAEENLNLPKMAEKDGCFOSGFNETCLVKIITGLLEEVYLEYIQNRFES 135
QY 118 SVINWDVMELLTKTGNDIOELNKLTKTHYSPKFDGRLGRLQGLKYVWRHPSFVYL 177
DB 136 SEQARAVQMSKTVLIQFLQKAKNLDATTPDPTNASLTLKLAQONQMLQDMTTHLIL 195
QY 178 SAMEKFAQAVRYL 191
DB 196 RSFKEFLQSSLRAL 209
```

```
RESULT 10
US-08-988-819-9
Sequence 9, Application US/08988819
Patent No. 6054294
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER DRIVE
```

```
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,819
FILING DATE: 12-DEC-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/792,019
FILING DATE: 03-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442A
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
NAME/KEY: Region
LOCATION: -30..0
US-08-988-819-9
```

```
Query Match 16.7%; Score 183; DB 3; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

QY 12 VGSLLVSGTRGKLPDAP-EFEKDL-----LIQRINMLMNVIDECFRLCYRT 57
DB 16 LGILLVLPAPAPVPPGEDSKDVAAPHROPJTSSERIDQIRYILDGISALRKETCKMS 75
QY 58 GICGKILEPAIFHLKLPAINDTDHGCLIGFNETSCLKLADGFEEFEVLEKFLTFEFGK 117
DB 76 NMCESSKEALAEENLNLPKMAEKDGCFOSGFNETCLVKIITGLLEEVYLEYIQNRFES 135
QY 118 SVINWDVMELLTKTGNDIOELNKLTKTHYSPKFDGRLGRLQGLKYVWRHPSFVYL 177
DB 136 SEQARAVQMSKTVLIQFLQKAKNLDATTPDPTNASLTLKLAQONQMLQDMTTHLIL 195
QY 178 SAMEKFAQAVRYL 191
DB 196 RSFKEFLQSSLRAL 209
```

```
RESULT 11
US-09-016-534-9
Sequence 9, Application US/09016534
Patent No. 6143874
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
APPLICANT: ELIOTT, GARY S.
APPLICANT: SARMIENTO, ULLA
APPLICANT: SENALDI, GIORGIO
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: ONE AMGEN CENTER
CITY: THOUSAND OAKS
STATE: CA
```

```

: COUNTRY: USA
: ZIP: 91320
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/016,534
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/792,019
: FILING DATE: 03-FEB-1997
: ATTORNEY/AGENT INFORMATION:
: NAME: COOK, ROBERT R.
: REGISTRATION NUMBER: 31,602
: REFERENCE/DOCKET NUMBER: A-442B
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: Protein
: LOCATION: 1..182
: FEATURE:
: NAME/KEY: Region
: LOCATION: -30...0
: US-09-016-534-9

```

```

Query Match          16.7% Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

```

```

QY 12 VCSLLVSGTRGKLPDP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
: ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 16 LGLLLVLPAPFAPVPBGDSKDVAPIHROPITSSERIDKQIRYLIDGISALRKETCNKS 75
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 GICKGLLEPAALFHLKIPAINPDHCGLIGFNETSGIKKLAGFPEFVLPKFLTTEGK 117
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 NNCESKKEALANNLPLPMARKDCPOSGFNETCLVLIITGLLEFEYLEYLQNRRES 135
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 118 SVINVDVMEELTKTGLWDIOEELNLTKTHTSPKFDRLGLRGLQKXYVHFAFYVL 177
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 136 SEQARAVQMSKTVLIQFLQKAKKNLDAITTPDPPTTNASLTKLQANQWLODMTHLIL 195
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 178 SAMEKFAQAVNL 191
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 196 RSKEFLQSLRAL 209
: | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 12
US-08-097-869-7
: Sequence 7, Application US/08097869
: Patent No. 6204364
: GENERAL INFORMATION:
: APPLICANT: Todaro, George J.
: TITLE OF INVENTION: HYBRID CYTOKINES
: NUMBER OF SEQUENCES: 8
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 545 Middlefield Road, Suite 200
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk

```

```

: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/097,869
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/753,178
: FILING DATE: 30-AUG-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24455-20001.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-813-5600
: TELEFAX: 415-327-2951
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 7:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-097-869-7

```

```

Query Match          16.7% Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

```

```

QY 12 VCSLLVSGTRGKLPDP-EFEKDL-----LIQRLNMLWVIDECFRLCYRT 57
: ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 16 LGLLLVLPAPFAPVPBGDSKDVAPIHROPITSSERIDKQIRYLIDGISALRKETCNKS 75
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 GICKGLLEPAALFHLKIPAINPDHCGLIGFNETSGIKKLAGFPEFVLPKFLTTEGK 117
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 76 NNCESKKEALANNLPLPMARKDCPOSGFNETCLVLIITGLLEFEYLEYLQNRRES 135
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 118 SVINVDVMEELTKTGLWDIOEELNLTKTHTSPKFDRLGLRGLQKXYVHFAFYVL 177
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 136 SEQARAVQMSKTVLIQFLQKAKKNLDAITTPDPPTTNASLTKLQANQWLODMTHLIL 195
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 178 SAMEKFAQAVNL 191
: | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 196 RSKEFLQSLRAL 209
: | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

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RESULT 13
US-08-795-473B-6
: Sequence 6, Application US/08795473B
: Patent No. 6217858
: GENERAL INFORMATION:
: APPLICANT: Galun, Elhan
: APPLICANT: Nahot, Orli
: TITLE OF INVENTION: A Pharmaceutical Composition for Treating
: TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Davidson, Davidson and Kappel, LLC
: STREET: 1140 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: USA
: ZIP: 10036
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5 inch disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: MS-DOS EDITOR
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/795,473B

```

```

: FILING DATE: 11-FEB-1997
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Davidson, Clifford M.
: REGISTRATION NUMBER: 32,728
: REFERENCE/DOCKET NUMBER: 963,1007
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212)-997-1028
: TELEFAX: (212)-997-1037
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 212 amino acids
: TYPE: amino acid
: TOPOLOGY: unknown
US-08-795-473B-6

```

```

Query Match          16.7%; Score 183; DB 4; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;

```

```

QY 12 VGSILVSGTRGKLPDAP-EFEKDL-----LIQRLMMMLWVIDECFRDLCYRT 57
: ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 LGLLLVPAFPAPVPPEGESKDYAAPHRQPLTSSERIDKQIRIILDGISALRKETCNKS 75
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 GICKGILEPAIFHLKLPAINDDHCGILGFNETSCIKLADGFEFEVLEFKPLTFEFGK 117
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 NMCSSKEALAEENNLNPKMAEKDGCFOSGFNEFTCLVKIITGLLEFEVLEYLQNRFFS 135
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 118 SYINVDVMEILLTGLGDIOEELNKLTKTHYSPKFDRLGLGRLOGIKYVVRHFAFYVL 177
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 136 SEQOARAVQGMSTVLIQFLQKAKKNLDAITTPPTTNASLITLQANQNLQDMTHLIL 195
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 178 SAMEKFAQAQAVRL 191
Db 196 RSFEKFLQSSLRAL 209

```

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RESULT 14
5510472-2
: Patent No. 5510472
: APPLICANT: REVEL, MICHEL, TILOLAIS, PIERRE
: TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
: INTERFERON-BETA2
: NUMBER OF SEQUENCES: 9
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/883,633
: FILING DATE: 15-MAY-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 208,925
: FILING DATE: 20-NOV-1980
: APPLICATION NUMBER: 449,447
: FILING DATE: 12-DEC-1989
: APPLICATION NUMBER: 860,883
: FILING DATE: 08-MAY-1986
: APPLICATION NUMBER: 208,925
: FILING DATE: 20-NOV-1980
: SEQ ID NO:2
: LENGTH: 212
5510472-2

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```

Query Match          16.7%; Score 183; DB 6; Length 212;
Best Local Similarity 25.8%; Pred. No. 4.7e-14;
Matches 50; Conservative 38; Mismatches 92; Indels 14; Gaps 2;
QY 12 VGSILVSGTRGKLPDAP-EFEKDL-----LIQRLMMMLWVIDECFRDLCYRT 57
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 16 LGLLLVPAFPAPVPPEGESKDYAAPHRQPLTSSERIDKQIRIILDGISALRKETCNKS 75
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 58 GICKGILEPAIFHLKLPAINDDHCGILGFNETSCIKLADGFEFEVLEFKPLTFEFGK 117
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 76 NMCSSKEALAEENNLNPKMAEKDGCFOSGFNEFTCLVKIITGLLEFEVLEYLQNRFFS 135

```

```

QY 118 SYINVDVMEILLTGLGDIOEELNKLTKTHYSPKFDRLGLGRLOGIKYVVRHFAFYVL 177
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 136 SEQOARAVQGMSTVLIQFLQKAKKNLDAITTPPTTNASLITLQANQNLQDMTHLIL 195
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 178 SAMEKFAQAQAVRL 191
Db 196 RSFEKFLQSSLRAL 209

```

```

RESULT 15
US-08-693-182-2
: Sequence 2, Application US/08693182
: Patent No. 5849283
: GENERAL INFORMATION:
: APPLICANT: CILIBERTO, Gennaro
: APPLICANT: SAVINO, Rocco
: APPLICANT: LAHN, Alvin
: TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
: TITLE OF INVENTION: SUPRAGONISTS, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
: TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
: TITLE OF INVENTION: MODELING
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Broadway and Neimark, P.L.L.C.
: STREET: 419 Seventh Street N.W., Ste. 300
: City: Washington
: STATE: D.C.
: COUNTRY: United States of America
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/693,182
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IT95/00216
: FILING DATE: 13-DEC-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IT RM 94A00805
: FILING DATE: 14-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BROWDY, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: CILIBERTO-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 184 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-693-182-2

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Query Match          16.6%; Score 182; DB 2; Length 184;
Best Local Similarity 25.6%; Pred. No. 5.1e-14;
Matches 42; Conservative 37; Mismatches 85; Indels 0; Gaps 0;
QY 28 PEFKDLIQLRLMMMLWVIDECFRDLCYRTGICKGILEPAIFHLKLPAINDDHCGILG 87
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 18 PLTSSERIDKQIRIILDGISALRKETCNKNMCSSKEALAEENNLNPKMAEKDGCFOSG 77
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 88 FNEISCLAKLADGFEFEVLEFKPLTFEFGKSYINVDVMEILLTGLGDIOEELNKLTKTH 147
: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 78 FNEFTCLVKIITGLLEFEVLEYLQNRFFESSEQOARAVQGMSTVLIQFLQKAKKNLDAIT 137

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Fri Oct 5 10:02:07 2001

us-09-230-048-2.raii

Page 8

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OY      148 YSPPKFDGII,LCRLQGLKTVWRHPASTYVLSAMEKFAQAGVRV 191
          | : |||| |:: : | : : | : : |
Db      138 TPDPETNSLLTKLQANQNLQMTTHILISFKFELQSSRLR 181

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Search completed: October 4, 2001, 19:10:32
Job time: 1163 sec

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•
•
•

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:48:59 ; Search time 44.98 Seconds
(without alignments)
345.478 Million cell updates/sec

Title: US-09-230-048-2

Sequence: 1 MCMFKLWLLVGSLLVSGT.....GQAVRVLDSIPDPVDPVHK 204

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	183	16.7	212	1 IVHUB2	Interleukin-6 prec
2	180.5	16.5	212	2 I46590	Interleukin 6 - pl
3	179.5	16.4	212	3 I46621	prointerleukin 6 -
4	173.5	15.8	208	2 T09216	Interleukin-6 prec
5	150	13.7	208	1 S29349	Interleukin-6 - sh
6	148	13.5	211	1 ICM56	Interleukin-6 prec
7	143.5	13.1	208	1 A56610	Interleukin-6 prec
8	134	12.2	211	2 A34247	Interleukin-6 prec
9	128	11.7	207	2 I46084	Interleukin 6 - ca
10	86.5	7.9	487	2 H69477	coenzyme F420--qui
11	85	7.8	408	2 A56186	cyclin E - African
12	82.5	7.5	447	1 UBMBDM	tubulin beta-1 cha
13	82.5	7.5	449	2 JQ1589	tubulin beta-5 cha
14	82.5	7.5	969	2 T41707	probable phenomene
15	82	7.5	367	2 T18185	probable site-spec
16	81.5	7.4	442	2 S00683	tubulin beta-1 cha
17	80.5	7.4	449	2 JQ1591	tubulin beta-7 cha
18	80	7.3	955	2 F84972	valine--CRNA ligas
19	79.5	7.3	451	2 S50747	beta-tubulin - pot
20	79.5	7.3	452	2 S50748	beta-tubulin - pot
21	79.5	7.3	1017	2 S67804	LMG1 protein - yea
22	79	7.2	385	2 T27626	hypothetical prote
23	78.5	7.2	445	2 JIA0048	tubulin beta-1 cha
24	78.5	7.2	674	2 T19495	hypothetical prote
25	77.5	7.1	609	2 S04757	NADH dehydrogenase
26	77.5	7.1	771	2 S51421	hypothetical prote
27	77	7.0	1004	2 B69483	hypothetical prote
28	77	7.0	1810	2 T30562	resistance protein
29	76.5	7.0	447	2 S17729	tubulin beta chain

30	76.5	7.0	447	2 S17730	tubulin beta chain
31	76.5	7.0	461	2 T39889	protein kinase - f
32	76	6.9	1005	2 B82969	sarcosine oxidase
33	75.5	6.9	164	2 T32824	hypothetical prote
34	75.5	6.9	260	2 D64246	DNA-directed DNA p
35	75.5	6.9	602	2 H86579	DNA gyrase subunit
36	75.5	6.9	602	2 C72043	DNA gyrase subunit
37	75.5	6.9	1158	2 T50454	probable rho1 GDP-
38	75	6.8	172	2 A46695	epididymal secreto
39	75	6.8	244	2 E72364	ABC transporter, A
40	75	6.8	333	2 B64380	hypothetical prote
41	75	6.8	505	1 S19169	cytochrome P450 2D
42	75	6.8	524	2 T43050	cyclin E - Caenorh
43	75	6.8	570	2 T30156	hypothetical prote
44	74.5	6.8	227	2 A70357	hypothetical prote
45	74.5	6.8	399	2 A84475	hypothetical prote

ALIGNMENTS

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N:Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
C:Accession: A32648; A25692; A26966; A33515; A25921; I52193; I56003; A27601;
R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A:Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A:Reference number: A32648; MUID:88082664
A:Accession: A32648
A:Molecule type: DNA
A:Residues: 1-212 <YAS>
A:Cross-references: GB:X04602; NID:g32949; PIDN:CAA68278.1; PID:g29495
A:Note: the authors translated the codon CAG for residue 130 as Glu
R:Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A:Title: Structure and expression of cDNA and genes for human Interferon-beta-2, a d1
A:Reference number: A91051; MUID:87053818
A:Accession: A25692
A:Molecule type: mRNA
A:Residues: 1-212 <ZIL>
A:Cross-references: GB:X04430; NID:g32673; PIDN:CAA28026.1; PID:g32674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Watanabe, Y.; Matsuda, T.; Kashimam
I., T.; Kishimoto, T.
Nature 324, 73-76, 1986
A:Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
A:Reference number: A9387; MUID:87065033
A:Accession: A26966
A:Molecule type: mRNA
A:Residues: 1-212 <HIR>
A:Cross-references: GB:X04602; NID:g33849; PIDN:CAA28268.1; PID:g33850
R:Totonouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A:Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A:Reference number: A33515; MUID:89391958
A:Accession: A33515
A:Molecule type: mRNA
A:Residues: 1-212 <TON>
A:Cross-references: GB:M29150; NID:g186349; PIDN:AA59154.1; PID:g307063
R:Heegman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A:Reference number: A25801; MUID:87004683
A:Accession: A25801
A:Molecule type: DNA; mRNA
A:Residues: 1-212 <HAE>
A:Cross-references: GB:X04403
A:Experimental source: fibroblast
R:May, L.T.; Hellgott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAV>
 A:Cross-references: GB:M1584; NID:9184628; PIDN:AAA52728.1; PID:9306910
 R:Wong, G.G.; Witek-Glancz, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: 152193; MUID:89193317
 A:Accession: 152193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:9186351; PIDN:AA41704.1; PID:9186352
 R:Birkenhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: 156003; MUID:88088768
 A:Accession: 156003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: GB:M18403; NID:9184631; PIDN:AAA52729.1; PID:9306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'X', 59-61, 'X', 63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takeuchi, K.; Hara, T.; Ishikawa, H.; An
 Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation f
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R:Wing, J.E.; Cornetti, C.; Steinman, R.M.; Crandall-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytokine T lymphocyte differentiation factor fo
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zapolsky, J.B.; Sengal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; MUID:91355644
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAV2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30k form contained both N-linked and O-linked carbohydrate; a 25k for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAV3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBIP:63787)
 A>Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R:Orlita, T.; Oheda, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; MUID:94266765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ide, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:116
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Intons: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-212/Product: interleukin-6, long form #status experimental <MAV>
 F:72-78,101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	16.7%	Score 183	DB 1	Length 212
Best Local Similarity	25.8%	Pred. No. 4.4e-10		
Matches	50	Conservative 38	Mismatches 92	Indels 14
Gaps	2			
12 VCSLWVGTRGKLPDAP-EPEKDL-----LIQRLNWMMLVIDECPRIQCYRT 57				
16 LGLLLVLPAAFPAPVPPEGDSKDVAAPIHNPOLTSERIDQIRYILDGISALRKETCNKS 75				
58 GICKGILPEPAIFHLKLPAINDTDCGLGFNETSCIKRIADGFEFEVLFKLTTFEPCK 117				
76 NMCESSKELAEENMLNLPMAEKDCGFQSGFNETGLVYKLTGLEFVYLEYLQIRFSS 135				
118 SYNVDMVELIKTKTLCMDIQLKTKTHYSPPKDRGLGRLQGLKQVWRFASFVYL 177				
136 SEQDARAVQMSKRVLLQFLQKKAKKNDATITPDPTTNASLTKIQANQNMIDMTTHLL 195				
178 SAMKFAQAVRVL 191				
196 RSKFEFLQSSLRAL 209				

RESULT 2
 146590
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: 146590
 R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A>Title: Expression of interleukin-6 in porcine, ovine, and bovine preimplantation co
 A:Reference number: 146590; MUID:92360284

RESULT 6

Interleukin-6 precursor mouse
N: Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocyte growth factor
C: Species: Mus musculus (house mouse)
C: Date: 30-Jun-1990 #sequence, revision 30-Jun-1990 #text, change 22-Jun-1999
C: Accession: A30531; A27610; A30571; S01323; S12103; E34047; A26662; A40486; A60799; S10
R: Tanabe, O.; Akita, S.; Kamihya, T.; Wong, G.C.; Hirano, T.; Kishimoto, T.
A: Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
A: Reference number: A30531; MUID:89035525
A: Accession: A30531
A: Molecule type: DNA
A: Residues: 1-211 <TAN>
A: Cross-references: GB:M20572; NID:g198369; PIDN:AAA39302.1; PID:g387386
R: Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Slin
Eur. J. Immunol. 18, 193-197, 1988
A: Title: cDNA cloning of murine interleukin-1p1: homology with human interleukin 6.
A: Reference number: A27610; MUID:88166883
A: Accession: A27610
A: Molecule type: mRNA
A: Residues: 1-211 <VAN>
A: Cross-references: GB:X06203; NID:g52701; PIDN:CA29560.1; PID:g52702
R: Mock, B.A.; Nordan, R.P.; Jettliffe, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cla
J. Immunol. 142, 1372-1376, 1989
A: Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A: Reference number: A30571; MUID:89124383
A: Accession: A30571
A: Molecule type: mRNA
A: Residues: 5-211 <MOC>
A: Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R: Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A: Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
A: Reference number: S01323; MUID:88329059
A: Accession: S01323
A: Molecule type: protein
A: Residues: 25-166, 'X', 168-211 <SIM>
R: Grenett, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455-1990
A: Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A: Reference number: S12103; MUID:91057159
A: Accession: S12103
A: Molecule type: mRNA
A: Residues: 1-211 <GRE>
A: Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R: Johnson, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A: Title: Interleukin amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A: Reference number: A90157; MUID:90147691
A: Accession: E34047
A: Molecule type: protein
A: Residues: 66-69, 'X', 71-75; 78-94; 128-148 <JAS>
R: Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhove, C.; Coulle, P.G.; Rubira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A: Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
A: Reference number: A26662; MUID:87092311
A: Accession: A26662
A: Molecule type: protein
A: Residues: 25-39, 'X', 41-42, 'X', 44-45 <VSN>
R: Chittu, C.P.; Moulds, C.; Coffman, R.L.; Kennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A: Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clon
A: Reference number: A40486; MUID:89017145
A: Accession: A40486
A: Molecule type: mRNA
A: Residues: 1-211 <CHI>
A: Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
R: Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
Blood 72, 2070-2073, 1988

A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is Interleukin-6
A:Reference number: A60799; MUID:89062753
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the Interleukin 6 gene in a
A:Reference number: S10241; MUID:90171860
A:Accession: S10241
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:g49738; PIDD:CA55824.1; PID:g581860
K:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A:Title: Specific covalent modification of the tryptophan residues in murine Interleu
A:Reference number: S38254; MUID:94039075
A:Accession: S38254
A:Status: preliminary
A:Molecule type: protein
A:Residues: 38-60;75, 'X', 77-79;176-203 <ZNA>
C:Genetics:
A:Gene: IL-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; Lymphokin
F:1-24/Domain: signal sequence; #status predicted <SIG>
F:25-211/Product: Interleukin-6; #status experimental <MAT>

Query Match	13.58;	Score 148;	DB 1;	Length 211;
Best Local Similarity	24.58;	Pred. No. 9,7e-07;		
Matches 47;	Conservative 35;	Mismatches 96;	Indels 14;	Gaps 3

[illegible]

RESULT 7

Interleukin-6 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A56610; S22162
R:Drögmans, U.; Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A:Title: Nucleotide sequence of bovine Interleukin-6 cDNA.
A:Reference number: A56610; MUID:93076003
A:Accession: A56610
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <R0>
A:Cross-references: EMBL:X57317; NID:q2193; PIDD:CA440572.1; PID:g2194
A:Experimental source: BIV induced B cell-lymphosarcoma
A:Note: sequence extracted from NCBI backbone (NCBIP:118917)
C:Superfamily: Interleukin-6
;Keywords: cytokine

[illegible]

```

C:Superfamily: Interleukin-6
A:Cross-references: GB:I16914; NID:g438519; PIDN:AAL16620.1; PID:g438520
Query Match      11.7%; Score 128; DB 2; Length 207;
Best Local Similarity 27.8%; Pred. No. 7.7e-05;
Matches 42; Conservative 29; Mismatches 62; Indels 18; Gaps 5;

QY 4 FRLMSLLLV-----GSLVSGTRGRKLPPDAPEEKDLLIQRLLMMMLAVIDECRDLCYR 56
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 14 FSLGLLVVAFAEPPTGGPLGDATSNRLPLTP---ADMDELLRYIIKGIISALKREKCDN 70
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
QY 57 TGICIGILEPAIFHLKIPIAINPDHCGILGFNETSCIKLADGFEEVLFKEFTFEF- 115
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 71 YNKCDSENLAENLNLPKLAENDGCRCGSFNOETCLTRTTGTGEOIYLKRLQDKYE 130
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
QY 116 ----GKSV-INVDVMELLTYTLGMDOIHEL 140
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 131 GDKENAKSVYTSTNVLLQLMKRKGN-ODEV 160
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

RESULT 10
HE9477
coenzyme F420--quinone oxidoreductase (EC 1.6.5.-) 53.9k chain AF1825 [similarity] -
N:Alternate names: F420HC--quinone oxidoreductase, 53.9k subunit nuom homolog
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 28-Jul-2000
C:Accession: H69477
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, E.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Nature 390, 364-370, 1997
A:Authors: Ulterback, T.; Cotton, M.D.; Springs, T.; Artlich, P.; Kaine, B.P.; Sykes, Smith, H.O.; Moese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archa
A:Reference number: A69250; MUID:98049343
A:Accession: H69477
A>Status: Preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-487 <KLE>
A:Cross-references: GB:A0000976; GB:A0000782; NID:g2689299; PIDN:AAB89424.1; PID:g264
C:Superfamily: NAOH dehydrogenase (ubiquinone) chain 4
C:Keywords: oxidoreductase

Query Match      7.9%; Score 86.5; DB 2; Length 487;
Best Local Similarity 21.4%; Pred. No. 1.9;
Matches 48; Conservative 40; Mismatches 79; Indels 57; Gaps 12;

QY 4 FRLMSLLLVGSLVSGTRGKLP-----DAPEEKDLL----IORLMMML-- 43
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 209 FTAMLLIFLGMLV-----KLPGIGHIMLPWAHAEPVPASALLPVLVLGAVLLRV 262
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
QY 44 WVIDCF-----RDLCYRTGICIGILEPAIFHLKIPIAINPDHCGILGFNETS----- 92
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 263 WMDSDFLDQYDIIIAIVASYIAGFSVRQK-----DYKRLAYSYVSQMGLVI 315
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
QY 93 ---CLKLADGEFEVEFLKLTTERFGKSVINVDVMEILLTKLGMDOIELNKKLRTH-Y 149
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 316 ALCL-----GSYGILGVVIOYISHAFGSKILFWTAGAIIASFRG--LRDIRMMSGMEHYV 368
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
QY 150 PKPDFRGILG--RIQGLKYWVHRFPASFVLSAMEKFACGAARVL 191
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
DB 369 PTIANNALLGFMTLSGT-LTIQMGEEFIILGLTTIYGFNLAVI 411
    |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |

RESULT 11
A56186
cyclin E - African clawed frog
N:Alternate names: cyclin E1
C:Species: Xenopus laevis (African clawed frog)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 16-Jul-1999
C:Accession: A56186; S34125
```

R:Rempel, R.E.; Sleight, S.B.; Maller, J.L.
 J. Biol. Chem. 270, 6843-6855, 1995
 A:Title: Maternal Xenopus Cdk2-cyclin E complexes function during meiotic and early embryonic development
 A:Reference number: A56186; MUID:95204484
 A:Accession: A56186
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-408 <REM>
 A:Cross-references: GB:123857; NID:9431745; PID:AAA73524.1; PID:9431746
 A:Contributor: A.: Philippe, M.
 A:Submitted to the EMBL Data Library, June 1992
 A:Description: Cloning and expression of Xenopus cyclin E.
 A:Reference number: 534125
 A:Accession: 534125
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-32, 'A', '34-199, 'NV', '202-258, 'GN', '261-408 <COU>
 A:Cross-references: EMBL:213966
 A:Superfamily: cyclin
 C:Keywords: cell cycle control

Query Match 7.8%; Score 85; DB 2; Length 408;
 Best Local Similarity 23.9%; Pred. No. 2.2; Mismatches 41; Indels 48; Gaps 10;
 Matches 37; Conservative 29;

QY 28 PHEKDLIQLRLMMMLWIDECFRLCYRTGIC---KGILEPAALFHLKPAINDTDC 83

DB 267 PQPQRIYIQ---IVQLDLCVLDIC---CLEYPCVLAASAWYHPSCELVK--- 314

QY 84 GLIGFET---SGLKRLADGFEFVLEKFLTEFGKSVIN---VDV----- 124

DB 315 -VSGKRVTELQCCIKWL-----VFPAMAIKCKGSKSLNFPKGVLDIADHNIQTHSGC 365

QY 125 MMLTFT-LGMDIOELNKLTKTH--VSPKPRFDR 155
 DB 366 LELMEKVIYNQALLLEQNTSPITGVLTPQSNK 400

RESULT 12

UBMUBM
 tubulin beta-1 chain - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999

C:Accession: J00275

R:Oppenheim, D.G.; Haas, N.; Silflow, C.D.; Snustad, D.P.

A:Title: The beta-tubulin gene family of Arabidopsis thaliana: preferential accumulation

A:Reference number: J00275; MUID:88255862

A:Accession: J00275

A:Molecule type: DNA

A:Residues: 1-447 <COP>

A:Cross-references: GB:M20405; NID:9166921; PID:AAA32893.1; PID:9166922

A:Note: the genome of A. thaliana contains a beta-tubulin gene family consisting of at 1

C:Genetics:

A:Insertions: 133/1; 223/1

C:Superfamily: tubulin

C:Keywords: microtubule

F:141-147/Region: tubulin/F142 GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif

Query Match 7.5%; Score 82.5; DB 1; Length 447;
 Best Local Similarity 23.8%; Pred. No. 4.2;
 Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

QY 12 VGSLLVSGTRGLPD-----APEFEKDLIQLRLMMMLW-----IDEC----- 49

DB 148 MGTLLSKIRREYPPRMLTFSPVSPKV-SPTVVEPVNATLSVHQLVENADECVLDNE 206

QY 50 -FRDLCTRTGICGKGLLEPAALFHLKPAINDTDCGLGFNETSC-----LKKL 97

DB 207 ALYDLCFRT-----LKLSTPFGDNLHLISATMSGVTCSLRPGQLNSDLRL 254

QY 98 ADGFEFEVLEKFLTEFGKSVINVDVMEELTKTGMD 135
 DB 255 AVNLIPFRLHFWMGFAPLTSRSGSQYISLVPELTQGM--WD 296

RESULT 13

J01589
 tubulin beta-5 chain - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 13-Aug-1999

C:Accession: J01589

R:Snustad, D.P.; Haas, N.A.; Kopecek, S.D.; Silflow, C.D.

A:Title: The small genome of Arabidopsis contains at least nine expressed beta-tubul

A:Reference number: J01587; MUID:92361268

A:Accession: J01589

A:Molecule type: DNA

A:Residues: 1-449 <SNU>

A:Cross-references: GB:M84702; NID:9166901; PID:AAA32883.1; PID:9166902

C:Genetics:

A:Gene: TUB5

C:Superfamily: tubulin

C:Keywords: microtubule

Query Match 7.5%; Score 82.5; DB 2; Length 449;
 Best Local Similarity 23.8%; Pred. No. 4.2;
 Matches 39; Conservative 21; Mismatches 49; Indels 55; Gaps 8;

QY 12 VGSLLVSGTRGLPD-----APEFEKDLIQLRLMMMLW-----IDEC----- 49

DB 148 MGTLLSKIRREYPPRMLTFSPVSPKV-SPTVVEPVNATLSVHQLVENADECVLDNE 206

QY 50 -FRDLCTRTGICGKGLLEPAALFHLKPAINDTDCGLGFNETSC-----LKKL 97
 DB 207 ALYDLCFRT-----LKLSTPFGDNLHLISATMSGVTCSLRPGQLNSDLRL 254

QY 98 ADGFEFEVLEKFLTEFGKSVINVDVMEELTKTGMD 135
 DB 255 AVNLIPFRLHFWMGFAPLTSRSGSQYISLVPELTQGM--WD 296

RESULT 14

T41707

probable phenomone response zinc proteinase (EC 3.4.24.-) - fission yeast (Schizosac

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000

C:Accession: T41707

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

A:Submitted to the EMBL Data Library, August 1998

A:Reference number: 222011

A:Accession: T41707

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-969 <MUR>

A:Cross-references: EMBL:AL031180; PID:CAA20142.1; GSPDB:GN00066

A:Experimental source: strain 972h-; cosmid c2E11 -chimeric

C:Genetics:

A:Gene: SPAC2E11.12c

A:Map position: 1

C:Superfamily: Insulysin

C:Keywords: hydrolase; metalloproteinase; zinc

F:68.72/Binding site: zinc (His) #status predicted

F:71/Active site: Glu #status predicted

QY 15 LTVSGTRGLPAPPEKDL-----LIQLRLMMMLWIDECFRLCYRTGICGKI 63

```

Db      73  LLEMGTK-KYPDENYRKYLESHNGISNATYASNNITYF-----EVSHDALY-----GA 121
QY      64  LEPAIAIFHL-----KLPAINDTDHGCLIGFNETSQLKLADGFEFEVLFFKELT 112
      122  LDRAQGFIDPLFLECKDEIRAV-DSEHC-----KNLQSDSNRFRLYSVLS 169
QY      113  TERGKSVI-----NVDVMEILTKTGMDIOEELNKLTKTHYSPPKFDRLGR--LQGL 164
      170  NP--KSVSKFNNGNIMETLADVPRKELGLDVROELKFEYDKYYSANIMKLVITIGREPLDVL 227
QY      165  KYWYRHFA 173
Db      228  QDMAAELEFS 236

```

RESULT 15

T18185

probable site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) - Chlorel

C/Species: Chlorella virus PCV-1

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T18185

R/Graves, M.V.; Van Etten, J.L.

submitted to the EMBL data library, May 1999

A/Reference number: Z18806

A/Accession: T18185

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-367 <GRA>

A/Cross-references: EMBL:U42580; NID:g4028896; PIDN:AAC96987.1

A/Experimental source: specific host Chlorella strain NC64A

C/Genetics:

A/Note: A683L

C/Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII

C/Keywords: methyltransferase; restriction modification system; S-adenosylmethionine

Query Match 7.58; Score 82; DB 2; Length 367;

Best Local Similarity 26.0%; Pred. No. 3.7;

Matches 32; Conservative 19; Mismatches 48; Indels 24; Gaps 3;

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QY      57  TGICGILPEPAIFHLKLPAINDTDHGCLIGFNETSQLKLADGFEFEVLFFKELTTERG 116
      217  TGLFTGDESSWKTTLPGALNGTEHKKMKGTJD----KVINGYENDVYSESRKEVA 271
QY      117  KSVINVDVMEILTKTGMDIOEELNKLTKTHYSPPKFDRLGRLOGLKWVRHSPFYV 176
      272  RAPLAINISVKKPR-----DIPKHNKGT-----LVDRKEMIKKYYWCTPCASTGT 312
Db      177  LSA 179
      313  ATA 315

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Search completed: October 4, 2001, 19:09:51
 Job time: 1252 sec

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Db 16 LGLLVLPAPFAPVLPBGDSKDVAPHSOPLTSSERIDKHIYIIDGIALRKETCNRS 75
 QY 58 GICKGLLEPAIAIFHLKLPAINDTDHGCLGFNFTSCLKLADGFFFEVLFKFLTTEFGK 117
 Db 76 NMCSEKSLAEANNLNPMAEKDGCFOGSEFEDTCLVKITGLLEFEVYLEYLOARFES 135
 QY 118 SVINVDVMEILTKTGLMDIOEELNKLTKTHYSPKPRDGLLGRLOGLKLYWVRHFAFVYL 177
 Db 136 SEBOARAVOMSTKVLIOFLQKKAKKNDAITTEPTTNASLTKLOAQONQMDMTTHLL 195
 QY 178 SAMEKFAQAVRYL 191
 Db 196 RSFKEFLQSSLRAL 209

RESULT 2
 IL6_CERTO STANDARD: PRT: 212 AA.

AC P46550:
 DT 01-NOV-1995 (rel. 32, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Cercopithecus locquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 NC NCBI_Taxid=9531;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJ.
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Bear S.S., Wayne A.E., Chikala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates."
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
 or send an email to license@sdb-sdb.ch).
 CC -----
 CC DR EMBL: L26032; AAA9972.1; .
 DR HSSP: P05231; IALU.
 DR InterPro: IPR001716; .
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PRO0433; IL6CSPMCF.
 DR PROSITE: PRO0434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KN Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 212 AA; 23668 MM; C73C035226BA4B9F CRC64;

QY 12 VGSLLVSTGRKLPDP-EFEKDL-----LIQRLNMLMVLVIDEGRDLCTRT 57
 Db 16 LGLLVLPAPFAPVLPBGDSKDVAPHSOPLTSSERIDKHIYIIDGIALRKETCNRS 75
 QY 58 GICKGLLEPAIAIFHLKLPAINDTDHGCLGFNFTSCLKLADGFFFEVLFKFLTTEFGK 117
 Db 76 NMCDSKSLAEANNLNPMAEKDGCFOGSEFEDTCLVKITGLLEFEVYLEYLOARFES 135
 QY 118 SVINVDVMEILTKTGLMDIOEELNKLTKTHYSPKPRDGLLGRLOGLKLYWVRHFAFVYL 177
 Db 136 SEBOARAVOMSTKVLIOFLQKKAKKNDAITTEPTTNASLTKLOAQONQMDMTTHLL 195
 QY 178 SAMEKFAQAVRYL 191
 Db 196 RSFKEFLQSSLRAL 209

RESULT 3
 IL6_HUMAN STANDARD: PRT: 212 AA.

AC P05231;
 DT 13-AUG-1987 (rel. 05, Created)
 DT 13-AUG-1987 (rel. 05, Last sequence update)
 DT 01-OCT-2000 (rel. 40, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)
 DE (INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).
 GN IL6 OR IFNB2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_Taxid=9606;
 [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87065033; PubMed=3491322;
 RA Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,
 RA Kashiwamura S.-I., Nakajima K., Koyama K., Iwanatsu A., Tsunagawa S.,
 RA Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;
 RT B lymphocytes to produce immunoglobulin."
 RL Nature 324:73-76(1986).
 CC [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88082664; PubMed=3500852;
 RA Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,
 RA Nakai S., Kishimoto T.;
 RT "Structure and expression of human B cell stimulatory factor-2
 (BSF-2/IL-6) gene."
 RL EMBO J. 6:2939-2945(1987).
 CC [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87067433; PubMed=3538015;
 RA May L.T., Helfgott D.C., Sehgal P.B.;
 RT "Anti-beta-interferon antibodies inhibit the increased expression of
 RT HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:
 RT structural studies of the beta 2 interferon involved."
 RL Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).
 CC [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87053818; PubMed=3023045;
 RA Zilberstein A., Ruggieri R., Koro J.H., Revel M.;
 RT "Structure and expression of cDNA and genes for human
 RT interferon-beta-2, a distinct species inducible by growth-stimulatory
 RT cytokines."
 RL EMBO J. 5:2529-2537(1986).
 CC [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88080768; PubMed=3320204;
 RA Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
 RA Aarden L.A.;
 RT "Molecular cloning and expression of hybridoma growth factor in
 RT Escherichia coli."
 RL J. Immunol. 139:4116-4121(1987).
 CC [6]

Query Match 16.7%; Score 183; DB 1; Length 212;
 Best Local Similarity 26.3%; Pred. No. 1.8e-10;
 Matches 51; Conservative 35; Mismatches 94; Indels 14; Gaps 2;

RP SEQUENCE FROM N.A.
 RX MEDLINE-89391958: PubMed-2789513:
 RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human B9F-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RA Blochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RP SEQUENCE FROM N.A.
 RC TISSUE-FIBROBLAST;
 RX MEDLINE-87004683: PubMed-3756081:
 RA Heegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Fiers W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [18]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89193317: PubMed-3266463:
 RA Mong G., Witek-Gianotti J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: Identification as a hematopoietic colony-stimulating
 RT factor.";
 RA Behring Inst. Mitt. 83:40-47(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93178270: PubMed-1291290:
 RA Chen Q.Y.;
 RT "Stable and efficient expression of human interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [10]
 RP SEQUENCE OF 30-63.
 RX MEDLINE-88154445: PubMed-7851440:
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [11]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE-95154344: PubMed-7851440:
 RA Breton J., Ja Fluzza A., Bertolero F., Orsini G., Valsasina B.,
 RA Zillicio R., de Filippis V., Polverino de Laureto P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [12]
 RP DISULFIDE BONDS.
 RX MEDLINE-89286115: PubMed-2472117:
 RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [13]
 RP MUTAGENESIS.
 RX MEDLINE-91243808: PubMed-2037043:
 RA Luetjicken C., Kruettgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [14]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96134845: PubMed-8555185:
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [15]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97303053: PubMed-9159484:

```

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.:
RT "Solution structure of recombinant human interleukin-6.";
RL J. Mol. Biol. 268:468-481(1997).
RN [161]
RX X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-97224126; PubMed-9118960;
RA Somers W., Stahl M., Seehra J.S.:
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling.";
RL EMBL J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC EMBL; X04430; CAA28026.1; -
CC DR EMBL; M14584; AAA52728.1; -
CC DR EMBL; X04602; CAA28368.1; -
CC DR EMBL; Y00081; CAA68378.1; -
CC DR EMBL; M18403; AAA52729.1; -
CC DR EMBL; M29150; AAA59154.1; -
CC DR EMBL; X04402; CAA27990.1; -
CC DR EMBL; X04403; CAA27990.1; -
CC DR EMBL; M54894; AAC41704.1; -
CC DR EMBL; S56892; AAD13886.1; -
CC DR EMBL; A09363; CAA00839.1; -
CC DR PIR; A32648; IVH02.
CC DR PIR; A25921; A25921.
CC DR PDB; 1IL6; 04-FEB-98.
CC DR PDB; 2TL6; 04-FEB-98.
CC DR PDB; 1ALU; 03-JUN-98.
CC MIM; 147620; -
CC DR InterPro; IPR001716; -
CC DR Pfam; PF004489; IL6; 1.
CC DR PRINTS; PRO0433; IL6GSPMCP.
CC DR PRINTS; PRO0434; INTERLEUKIN6.
CC DR PROSITE; PS00254; INTERLEUKIN_6; 1.
CC KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
CC FT SIGNAL 1 29
CC FT CHAIN 30 212
CC FT DISULFID 72 78
CC FT DISULFID 101 111
CC FT CARBOHYD 73
CC FT MUTAGEN 173 173
CC FT MUTAGEN 185 185
CC FT MUTAGEN 204 204
CC FT MUTAGEN 210 210
CC FT MUTAGEN 212 212
CC SQ SEQUENCE 212 AA; 23718 MW; 1FED1FE1B734079 CRC64;
CC -----
CC Query Match 16.7%; Score 183; DB 1; Length 212;
CC Best local similarity 25.8%; Pred No.1.8e-10;
CC Matches 50; Conservativity 38; Mismatches 92; Indels 14; Gaps 2;
CC -----
CC 12 VSSLVSGTGRGLPDAP-EFENDL-----LIQRLNMLMWIDECFRDLCYRT 57
CC : ||||| | | | | | : : : : : : : : : : : : : : : : : : :
CC 16 LGLLLVLPAPAPVPPGDSKDVAAPIHQPLTSSBRIDKQIRYLIDGTSALRKETCKNS 75
CC : : : : : | | | | | : : : : : : : : : : : : : : : : : : :
CC 58 GICKGILPEALAFHLKLPAINDTDHCGILGFNETSCKLKADGFEFEVLAFFLTTEGK 117
CC : : : : : | | | | | : : : : : : : : : : : : : : : : : : :
CC 76 NCSCSEKELANNNNLNLPMAEKDCGFSGFNEETCLVIITIGLEFFEYVLELQNNRES 135

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OY 118 SVINVDWMLTTTCLMDIOBELNKTKHYSPKFDRLGLGRLQKLYWRHFRASFYVL 177
 DB 136 SEBOARAVOMSTKVLIOFLQKAKANLDAITTPPTTNASLITKLQANONMLQDMTHLIL 195
 OY 178 SAMEKFAQAQAVRVL 191
 DB 196 RSFEKFLQSLRAL 209

RESULT 4

IL6_MACMU STANDARD; PRT; 212 AA.
 ID IL6_MACMU
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RAC 2;
 RA MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 RT nonhuman primates."
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC
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 CC
 CC EMBL: L26028; AAA99978.1; -
 CC HSSP: P05231; IALU.
 CC InterPro: IPR001716; -
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6CSFNGF.
 CC DR PROSITE: PS00254; INTERLEUKIN6.
 CC DR CYCLOKINE; Glycoprotein; Growth factor; Signal.
 CC KW SIGNAL 1 29 BY SIMILARITY.
 CC FT CHAIN 1 29 INTERLEUKIN-6.
 CC FT DISULFID 72 78 POTENTIAL.
 CC FT CARBOHYD 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SO SEQUENCE 212 AA; 23728 MW; 4130DF0CF0BCAD CRC64;

Query Match

Best Local Similarity 16.5%; Score 181; DB 1; Length 212;
 Matches 50; Conservative 40; Mismatches 98; Indels 8; Gaps 2;

OY 4 FKLMSLLVLSL-----LVSGTCKGLPDAPRFE-----KDLILQRLNMLAVIDECFDLCY 55
 DB 14 FSLGGLLVLPAPVLPAPVLPAGEDESKNAAPHSQLTSSERIDKIRYILGLISALRKETCN 73
 OY 56 RTGICGILPEPAIPIHLKPAINDTDHGLIGFENRTSCLKILADGFEFEVLEKFLTTEE 115

DB 74 RSNMCESSKEALNENLNLPKNAEKDCGCGFNEPDTCLVKTITGILEFEVLEYLQNR 133
 OY 116 GKSIVVDWMLTTTCLMDIOBELNKTKHYSPKFDRLGLGRLQKLYWRHFRASFY 175
 DB 134 ESSEBOARAVOMSTKVLIOFLQKAKANLDAITTPPTTNASLITKLQANONMLQDMTHLIL 193
 OY 176 VISAMEKFAQAQAVRVL 191
 DB 194 ILSRFEKFLQSLRAL 209

RESULT 5

IL6_PIG STANDARD; PRT; 212 AA.
 ID IL6_PIG
 AC P26893;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=91338547; PubMed=1873476;
 RA Richards C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 RT expression of mRNA in synovial fibroblasts in vitro."
 RL Cytokine 3:269-276(1991).
 CC
 CC SEQUENCE FROM N.A.
 CC MEDLINE=92360284; PubMed=1497880;
 CC Mathialagan N., Bixby J.A., Roberts M.R.;
 RA "Expression of interleukin-6 in porcine, ovine, and bovine
 RT preimplantation conceptuses."
 RL Mol. Reprod. Dev. 32:324-330(1992).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC
 CC EMBL: M86722; AAC37333.1; -
 CC HSSP: M80258; AAC37127.1; -
 CC HSSP: P05231; IALU.
 CC InterPro: IPR001716; -
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6CSFNGF.
 CC DR PROSITE: PS00254; INTERLEUKIN6.
 CC DR CYCLOKINE; Glycoprotein; Growth factor; Signal.
 CC KW SIGNAL 1 29 BY SIMILARITY.
 CC FT CHAIN 1 29 INTERLEUKIN-6.
 CC FT DISULFID 72 78 BY SIMILARITY.
 CC FT DISULFID 101 111 BY SIMILARITY.
 CC FT CONFLICT 30 30 G->E (IN REF. 2).
 CC SO SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match

Best Local Similarity 16.4%; Score 179.5; DB 1; Length 212;
 Matches 23.9%; Pred. No. 3.8e-10;


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CC -----
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL: I46803; AAB01429.1; -.
DR HSSP: P05231; 1ALU.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN 21
FT CHAIN 22
FT DISULFID 64
FT DISULFID 70
FT DISULFID 93
FT CARBOHYD 164
FT SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 14.2%; Score 155.5; DB 1; Length 205;
Best Local Similarity 21.1%; Pred. No. 7.3e-08;
Matches 42; Conservative 46; Mismatches 96; Indels 15; Gaps 3;

QY 8 SLLVSLVSGTGRKLPD-APEFEDLIQRL-----NMMLVYDCECFDL 53
D 4 SAEISGLLVATAPTPPGPLGDEKDDTSRLYLSPOKTEALIKYILKISAMREEM 63
QY 54 CYRFGICGKILGPAIFHLKPAINDVHGLIGFNETSCIKLADGFEEVLEKFLTT 113
D 64 CEKDKCKENSEALAEENLNIPKAEKDGCSQSPNOTCMLRTTGLLEYQIYLDIYON 123
QY 114 EFGKSVINVDVMELLTFTLGMIDIOELNKLKTHYSPKPRGILGRGLGKLVWRHFA 172
D 124 EYEGDKKAIKAVQISKALQILRKVKNPDEVTPPTNANSLMNNLQSQNDMMKNTK 183
QY 173 SFYLSAMEKFAGOAVRVL 191
D 184 IILIRSLNFIQFSLRAI 202

RESULT 10
ID IL6_CAPHI STANDARD; PRT; 208 AA.
AC Q28319;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97392354; PubMed=9250586;
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect
RT cells.";
RL Int. Arch. Allergy Immunol. 113:409-416(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----
DR EMBL: D86569; BAA13118.1; -.
DR HSSP: P05231; 2IL6.
DR InterPro: IPR001716; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PRINTS: PR00434; INTERLEUKIN_6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN 29
FT CHAIN 30
FT DISULFID 72
FT DISULFID 78
FT DISULFID 101
FT CARBOHYD 38
FT SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 13.9%; Score 152; DB 1; Length 208;
Best Local Similarity 26.2%; Pred. No. 1.6e-07;
Matches 37; Conservative 31; Mismatches 69; Indels 4; Gaps 1;

QY 51 RDLCYRFGICGKILGPAIFHLKPAINDVHGLIGFNETSCIKLADGFEEVLEKFL 110
D 69 KEICEKDEKENSEKTELAEENLNKLPKMEKDGCSQSPNQALIKLTAGILEYQIYLD 128
QY 111 LTTEFGKSVINVDVMELLTFTLGMIDIOELNKLKTHYSPKPRGILGRGLGKLVWRH 170
D 129 LQNEEGQETVMEIQSSIRFLIOILKEKTAGLITTT-----PATVDMLEKQSSNEWKN 184
QY 171 FAEFYLSAMEKFAGOAVRVL 191
D 185 AKVYIILIRSLNFIQFSLRAI 205

RESULT 11
ID IL6_SHEEP STANDARD; PRT; 208 AA.
AC P28455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94041419; PubMed=8225400;
RA Andrews A.E., Barcham G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RT "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA.";
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ebrahimi B.;
RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

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CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC DR EMBL: X62501; CAA44363.1; -
CC DR EMBL: X68723; CAA48662.1; -
CC DR EMBL: A19159; CAA01443.1; -
CC DR PIR: S29549; S29549.
CC DR HSSP: P05231; 2116.
CC DR InterPro: IPR001716; -
CC DR Pfam: PF00489; IL6; 1.
CC DR PRINTS: PR00433; L6GCSFMC.
CC DR PRINTS: PR00434; INTERLEUKIN6.
CC DR PROSITE: PS00254; INTERLEUKIN6_1.
CC DR Cytokine; Glycoprotein; Growth factor; Signal.
CC KW SIGNAL 1 29 BY SIMILARITY.
CC FT CHAIN 30 208 INTERLEUKIN-6.
CC FT DISULFID 72 78 BY SIMILARITY.
CC FT DISULFID 101 111 BY SIMILARITY.
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CONFLICT 4 4 L -> R (IN REF. 2).
CC FT CONFLICT 110 110 I -> V (IN REF. 2).
CC FT CONFLICT 171 171 M -> L (IN REF. 2).
CC FT CONFLICT 201 201 S -> R (IN REF. 2).
CC FT CONFLICT 201 201 S -> R (IN REF. 2).
CC SQ SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 13.7%; Score 150; DB 1; Length 208;
Best Local Similarity 26.2%; Pred. No. 2.5e-07;
Matches 37; Conservative 30; Mismatches 70; Indels 4; Gaps 1;

QY 51 RDLCTRTGICKLEPAALFHLKLPAINDTDHCGLIGNETSCLKLADGFEFEVLERF 110
DB 69 KETCEINDECEENSKETLAKENKLPMEKDCFOGFGNAICLITTTAGLEYOIYDF 128
QY 111 LTFEPKSVINVDVMEELLTKTLGMDIOEELNK/TKTHYSPKPRDRLGLRLOGLKQVWH 170
DB 129 LQNEFGNGETWELLOSSIRTLIQILKEKIAGLITT-----PATHTDMLKMOSSNEMVKN 184
QY 171 EASFVYLAMEKFAQAVRL 191
DB 185 AKVITILRLSENFLOPSLRAI 205

RESULT 12
IL6_MOUSE STANDARD: PRT; 211 AA.
ID IL6_MOUSE
AC P08505;
DT 01-AUG-1988 (rel. 08, Created)
DT 01-AUG-1988 (rel. 08, Last sequence update)
DT 15-JUL-1998 (rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (INTERLEUKIN HP-1) (B-CELL HYBRIDOMA
DE GROWTH FACTOR).
DE IL6 OR IL-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RX MEDLINE-8816683; PubMed-2965020;
RA van Snick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,
RA Boon T., Simpson R.J.;
RA "cDNA cloning of murine Interleukin-HP1: homology with human
RA Interleukin 6.";
RA Eur. J. Immunol. 18:193-197(1988).
RN [2]

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RP SEQUENCE FROM N.A.
RX MEDLINE-89035525; PubMed-3263439;
RA Tanabe O., Akira S., Kamita T., Wong G.G., Hirano T., Kishimoto T.;
RT "Genomic structure of the murine IL-6 gene. High degree conservation
RT of potential regulatory sequences between mouse and human.";
RL J. Immunol. 141:3875-3881(1988).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-91057159; PubMed-2243807;
RA Grenett H.E., Fuentes N.L., Fuller G.M.;
RT "Cloning and sequence analysis of the cDNA for murine Interleukin-6.";
RL Nucleic Acids Res. 18:6455-6455(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-89017145; PubMed-3262872;
RA Chiu C.-P., Moulds C., Coffman R.L., Rennick D., Lee F.;
RT "Multiple biological activities are expressed by a mouse Interleukin
RT 6 cDNA clone isolated from bone marrow stromal cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).
RN [5]
RP SEQUENCE OF 5-211 FROM N.A.
RC STRAIN-C57BL/6J;
RX MEDLINE-89124383; PubMed-2563387;
RA Mock B.A., Nordan R.P., Justice M.J., Kozak C., Jenkins N.A.,
RA Copeland N.G., Clark S.C., Wong G.G., Rudikoff S.;
RT "The murine IL-6 gene maps to the proximal region of chromosome 5.";
RL J. Immunol. 142:1372-1376(1989).
RN [6]
RP SEQUENCE OF 1-6 FROM N.A.
RC STRAIN-BALB/C;
RX MEDLINE-90171860; PubMed-2106569;
RA Blankenstein T., Qin Z., Li W., Diamantstein T.;
RT "DNA rearrangement and constitutive expression of the Interleukin 6
RT gene in a mouse plasmacytoma.";
RL J. Exp. Med. 171:965-970(1990).
RN [7]
RP SEQUENCE OF 25-211.
RX MEDLINE-88329059; PubMed-3262059;
RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
RT sequence and relation to human Interleukin-6.";
RL Eur. J. Biochem. 176:187-197(1988).
RN [8]
RP SEQUENCE OF 66-75; 78-84 AND 128-148.
RX MEDLINE-90147691; PubMed-2302197;
RA Jahnke W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
RT "Internal amino acid sequencing of proteins by in situ cyanogen
RT bromide cleavage in polyacrylamide gels.";
RL Biochem. Biophys. Res. Commun. 166:159-145(1990).
RN [9]
RP SEQUENCE OF 25-45.
RX MEDLINE-87092311; PubMed-2948184;
RA van Snick J., Cayphas S., Vink A., Uyttenhove C., Coule P.G.,
RA Rubira M.R., Simpson R.J.;
RT "Purification and NH2-terminal amino acid sequence of a
RT T-cell-derived lymphokine with growth factor activity for B-cell
RT hybridomas.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
RN [10]
RP FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
DR EMBL; X06203; CAA29560.1; -
DR EMBL; M20572; CAA39302.1; -
DR EMBL; X51457; CAA35824.1; -
DR EMBL; J03783; CAA39301.1; -
DR EMBL; X54542; CAA38411.1; -
DR EMBL; M24221; CAA68814.1; -
DR PIR; A30531; ICMS6.
DR HSSP; P05231; IALU.
DR MGD; MGI:965559; IL6.
DR InterPro: IPR001716; -
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFGE.
DR PRINTS; PR00434; INTERLEUKIN.
DR PROSITE; PS00254; INTERLEUKIN.6; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 211 INTERLEUKIN-6.
FT DISULFID 70 76 BY SIMILARITY.
FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24384 MM; BBB47DDA9E86787A CRC64;

```

```

Query Match 13.58; Score 148; DB 1; Length 211;
Best Local Similarity 24.58; Pred. No. 3.9e-07;
Matches 47; Conservative 35; Mismatches 96; Indels 14; Gaps 3;

```

```

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U12234; CAA83030.1; -
DR HSSP; P05231; 2IL6
DR InterPro: IPR001716; -
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFGE.
DR PRINTS; PR00434; INTERLEUKIN.6.
DR PROSITE; PS00254; INTERLEUKIN.6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 207
FT CHAIN 7 207 INTERLEUKIN-6.
FT DISULFID 67 73 BY SIMILARITY.
FT DISULFID 96 106 BY SIMILARITY.
SQ SEQUENCE 207 AA; 22945 MM; 45540154EA9C0F50 CRC64;

```

```

Query Match 13.28; Score 144.5; DB 1; Length 207;
Best Local Similarity 23.98; Pred. No. 8.3e-07;
Matches 48; Conservative 37; Mismatches 99; Indels 17; Gaps 3;

```

```

OY 12 VGLLVSGT-----RGKL-----PDAPFENKLLIQRLNMMWVDECFRDL CYRTG 58
DB 15 LGMLVTTAAPTQSVRRGDEDTEDTPRPPVYTTSSQVGLLTHVMEVEMKRELCKGNS 74
OY 59 ICKGLEPAALFHLKLPAINDTDHGCLIGFNETSCCLKLADGFFEEVLFKEFLTEF-GK 117
DB 75 DOMNDDALAEENKLPFQIRNDGCGYGYNGEICKLKISSGLLEHYSLYELMKNNLNDN 134
OY 118 SVINVDVWELLTKTIGMDIOBELNKLTKTHYSPKFDRLGLRGLGKYWRHFASEFVL 177
DB 135 KKDKARVQROPTETLIHFNEQVKDLHKIVLPPTISNALTLTKLESQKEMLTETKIQFPL 194
OY 178 SAMEKFAQAVR 189
DB 195 KSLPEFLKVTLR 206

```

```

RESULT 13
IL6_CANFA
ID IL6_CANFA STANDARD: PRT: 207 AA.
AC P41323.
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MONGREL;
RX MEDLINE=94303924; PubMed=7913298;
RA Kufelka G.L., Youker R.A., Hawkins H.K., Perrard J.L.,
RA Michael L.H., Ballantyne C.M., Smith C.W., Entman M.L.;
RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
RT reperfusion.";
RL Ann. N.Y. Acad. Sci. 723:258-270(1994).

```

```

CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC ACTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----

```

```

OY 8 SLLVGLSVGSTRKLR-----DA-----PEFKDILLIQRLNMMWVDECFRDL 53
DB 7 SAFSGLLVMTAAPTQSVRRGDEDTEDTPRPPVYTTSSQVGLLTHVMEVEMKRELCKGNS 66
OY 54 CYRTGICGILEPAALFHLKLPAINDTDHGCLIGFNETSCCLKLADGFFEEVLFKEFLTEF 113
DB 67 CDKFKKCDSDNEALAEENKLPFQIRNDGCGYGYNGEICKLKISSGLLEHYSLYELMKNNLNDN 126
OY 114 EFGKSVINVDVWELLTKTIGMDIOBELNKLTKTHYSPKFDRLGLRGLGKYWRHFASEFVL 173
DB 127 NYEGDKENVKSVHMKTKLVOMLKSQKVNODEVTTPTDPTASLQALISODECVKHTTI 186
OY 174 FYVLAME---KFAQAVRVL 191
DB 187 HLILNLEDFLOFSLRVIRM 207

```

```

RESULT 14
IL6_BOVIN
ID IL6_BOVIN STANDARD: PRT: 208 AA.
AC P26892.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HOLSTEIN;
RX MEDLINE=93076003; PubMed=1446077;
RA Drocmanis L., Cludts I., Cleuter Y., Kettmann R., Bury A.;
RT "Nucleotide sequence of bovine Interleukin-6 cDNA.";
RL DNA Seq. 2:411-413(1992).

```

```

CC -I- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC ACTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -I- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:08 ; Search time 54.44 Seconds
(Without alignments)
21.158 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105
Perfect score: 103
Sequence: 1 GFNETSCUKLADGFFEEFEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/geneseq/AA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/geneseq/AA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/geneseq/AA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/geneseq/AA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/geneseq/AA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/geneseq/AA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/geneseq/AA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/geneseq/AA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/geneseq/AA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/geneseq/AA1989.DAT:*
11: /SIDSI/gcgdata/geneseq/geneseq/AA1990.DAT:*
12: /SIDSI/gcgdata/geneseq/geneseq/AA1991.DAT:*
13: /SIDSI/gcgdata/geneseq/geneseq/AA1992.DAT:*
14: /SIDSI/gcgdata/geneseq/geneseq/AA1993.DAT:*
15: /SIDSI/gcgdata/geneseq/geneseq/AA1994.DAT:*
16: /SIDSI/gcgdata/geneseq/geneseq/AA1995.DAT:*
17: /SIDSI/gcgdata/geneseq/geneseq/AA1996.DAT:*
18: /SIDSI/gcgdata/geneseq/geneseq/AA1997.DAT:*
19: /SIDSI/gcgdata/geneseq/geneseq/AA1998.DAT:*
20: /SIDSI/gcgdata/geneseq/geneseq/AA1999.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	100.0	19	AAW23945	Human herpesvirus
2	103	100.0	185	AAW5015	Kaposi's sarcoma h
3	103	100.0	204	AAW74570	Kaposi sarcoma her
4	103	100.0	204	AAW40103	Human herpesvirus
5	103	100.0	204	AAW23944	Human herpesvirus
6	61	59.2	162	AAW7391	Human mutant IL-6a
7	61	59.2	162	AAW00131	Human interleukin-
8	61	59.2	163	AAW00132	Human interleukin-
9	61	59.2	167	AAW72649	Human interleukin-
10	61	59.2	169	AAW7387	Human IL-6 mutant
11	61	59.2	174	AAW5342	Hybrid human cyto

12	61	59.2	176	AAW5341	Hybrid human cyto
13	61	59.2	177	AAW7388	Human IL-6 mutant
14	61	59.2	179	AAW5334	Human interleukin-
15	61	59.2	183	AAW60125	Human interleukin
16	61	59.2	184	AAW81158	Polypeptide with B
17	61	59.2	184	AAW94753	Sequence of varian
18	61	59.2	184	AAW0532	Human B-cell stiml
19	61	59.2	184	AAW03914	Polypeptide with h
20	61	59.2	184	AAW20783	Interleukin-6. A
21	61	59.2	184	AAW72219	Human interleukin-
22	61	59.2	184	AAW54990	Mutant interleukin
23	61	59.2	184	AAW55256	Interleukin-6. Ho
24	61	59.2	184	AAW4659	Interleukin-6 for
25	61	59.2	184	AAW68623	B-cell differentia
26	61	59.2	184	AAW07199	Human interleukin
27	61	59.2	184	AAW07200	Human interleukin
28	61	59.2	184	AAW07201	Human interleukin
29	61	59.2	184	AAW07197	Human interleukin
30	61	59.2	184	AAW07198	Human interleukin
31	61	59.2	184	AAW02609	Interleukin-6. Ho
32	61	59.2	184	AAW02610	Interleukin-6 (Q75
33	61	59.2	184	AAW02611	Interleukin-6 (Q75
34	61	59.2	184	AAW02612	Interleukin-6 (Q75
35	61	59.2	184	AAW08476	Interleukin-6 vari
36	61	59.2	184	AAW08477	Interleukin-6 vari
37	61	59.2	184	AAW08478	Human interleukin
38	61	59.2	184	AAW58518	Human interleukin
39	61	59.2	184	AAW58519	Human interleukin
40	61	59.2	184	AAW92803	Human IL-16 mutleu
41	61	59.2	185	AAW81159	Polypeptide with B
42	61	59.2	185	AAW90059	Human Ala B cell d
43	61	59.2	185	AAW94754	Sequence of varian
44	61	59.2	185	AAW91015	Synthetic interlev
45	61	59.2	185	AAW05275	Segment of human B

ALIGNMENTS

RESULT 1
ID AAW23945 standard; Protein: 19 AA.
AC AAW23945;
XX
XX 01-JUL-1998 (first entry)
DE Human herpesvirus 8 Interleukin-6 fragment.
XX
XX Interleukin-6; IL-6; human herpesvirus 8; HHV8;
KW shotgun-cloning; Antibodies; diagnosis; treatment.
XX
OS Human herpesvirus 8.
XX
XX
XX W09803657-A1.
XX
XX 29-JAN-1998.
XX
XX
XX 19-JUL-1996; 96WO-EP03199.
XX
XX 19-JUL-1996; 96WO-EP03199.
XX
XX 19-JUL-1996; 96WO-EP03199.
XX
XX (BEHW) BEHRING DIAGNOSTICS GMBH.
XX (UYNV) UNIV NEW YORK STATE.
XX
XX Albrecht J, Fleckenstein B, Friedman-klen A, Huang Y;
XX Netpel F;
XX
XX WPI; 1998-120781/11.
XX
XX Viral interleukin-6 produced recombinantly from human herpes virus 8
XX DNA - and related nucleic acid and antibodies, used for diagnosis
XX and treatment of herpes 8 infection or related diseases, e.g. Kaposi

PT	sarcoma
XX	
PS	
Claim 4;	Page 8; 19pp; English.
XX	
CC	The interleukin-6 (IL-6) fragment and protein ANW23944 can be used to detect antibodies and antibodies can be used to detect IL-6. This can be used for the diagnosis of HHV8 infection or associated diseases such as Kaposi sarcoma or kidney cell carcinoma. Antibodies, proteins and the gene sequence can all be used in the treatment of infections and diseases as mentioned above.
CC	
CC	
XX	
SO	Sequence 19 AA;
Query Match	100.0%; Score 103; DB 19; Length 19;
Best Local Similarity	100.0%; Pred. No. 2.6e-10;
Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 GPNFTSCLTKLADGFEFE 19 1 gfnetsclktkladgllfete 19
DB	

XX	RESULT	2
XX	AAW95015	
XX	AAW95015	standard; peptide: 185 AA.
XX	AAW95015:	
XX	21-MAY-1999	(first entry)
XX	Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.	
XX	Cytokine: interleukin-B30; IL-B30; forensic science: cell proliferation	
XX	Inflammatory condition; drug screening; human; IL-6.	
XX	Kaposi's sarcoma herpes virus.	
XX	WO9905280-A1.	
XX	04-FEB-1999.	
XX	24-JUL-1998;	98WO-US15423.
XX	25-JUL-1997;	97US-090905.
XX	(SCHE) SCHERING CORP.	
PA	Bazan JF;	
XX	WI: 1999-142935/12.	
XX	Newly isolated or recombinant polynucleotide encoding mammalian	
XX	cyclokin interleukin-B30 (IL-B30), including fragments - useful for	
XX	regulating activation, development, differentiation and function of	
XX	various cell types, and for diagnosing and treating conditions	
XX	associated with IL-B30	
XX	Disclosure: Page 11-12: 83pp: English.	
XX	This invention relates to mammalian cytokine interleukin-B30 (IL-B30)	
XX	polypeptides. Host cells containing a vector comprising the IL-B30	
XX	nucleic acids are used for the recombinant production of the proteins.	
XX	The polynucleotides are useful for diagnosis of IL-B30 mediated	
XX	conditions, and forensic science (e.g. to distinguish rodent from human	
XX	or as a marker to distinguish between different cells exhibiting	
XX	differential expression or modification patterns). The IL-B30 (including	
XX	fragments), together with antibodies that bind to IL-B30 are useful for	
XX	teaching purposes. They are also used for treating conditions associated	
XX	with abnormal physiology or development, including inflammatory	
XX	conditions. The polypeptide cytokine should mediate cytokine synthesis	
XX	and proliferation in cells. IL-B30 is useful for drug screening to	
XX	identify compounds having binding affinity to IL-B30. The present	

CC	sequence represents a kaposi's sarcoma herpes virus IL-6
XX	
SQ	Sequence 185 AA;

Query Match	100.0%	Score 103	DB 20	Length 185
Best Local Similarity	100.0%	Pred. No. 2	7e-09	
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GFNETSCLKLAGDGFEE	19	
DB	68	ginecsclkladgffere	86	

Query Match	Best Local Similarity	100.0%	Score 103	DB 19	Length 204
Matches 19	Conservative 0	Mismatches 0	Indels 0	Gaps 0	

OY 1 GFNETSCLKRIADGFEFE 19
 Db 87 gfnetsclickiadgffefe 105

RESULT 4

AAW40103
 ID AAW40103 standard; Protein; 204 AA.

XX AAW40103;

XX 15-JUL-1998 (first entry)

XX Human herpesvirus 8 (HHV-8) interleukin-6.

XX DL-B: thymidylate synthase; dihydrofolate reductase; primer: HHV-8;
 KM Bcl-2 homologue; IE-1a; IE-1B; viral macrophage inhibitory protein;
 KM Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; vIL-6.

XX Kaposi's sarcoma associated herpesvirus.

XX MO9804284-A1.

XX 05-FEB-1998.

XX 24-JUL-1997; 97MO-US12931.

XX 25-JUL-1996; 96US-0022591.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Hardwick JM, Hayward GS, Nicholas J, Reitz MR;

XX WPI: 1998-130422/12.

XX New human herpes virus gene region containing 8 open reading frames
 PT - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based
 PT large cell lymphoma

XX Claim 1; Pages 59-60; 84pp; English.

XX The sequence represents a novel human herpesvirus 8 (HHV-8)
 CC Interleukin-6. The invention claims for novel genes, which includes
 CC the viral interleukin-6 gene, found at the divergent DL-B locus. HHV-8
 CC divergent locus DL-B lies between open reading frames 11 and 17.
 CC Sequencing of the HHV-8 divergent locus DL-B revealed the presence of
 CC nine viral ORFs with gene products related to cellular proteins. These
 CC proteins include the thymidylate synthase (TS, AAW40100), dihydrofolate
 CC reductase (DHFR, see AAW40101), Bcl-2 homologue (AAW40102), IE-1A
 CC (AAW40107), IE-1B (AAW40108) and, four cytokines which include viral
 CC interleukin-6 (vIL-6), viral macrophage inhibitory protein (vMIP)-1A
 CC (AAW40104) and -1B (AAW40105) and beta-chemokine-like (BCK, AAW40106)
 CC protein. The invention claims the mentioned proteins and a
 CC polynucleotide containing HHV-8 genes encoding one or more of these
 CC proteins. The invention also claims that the polynucleotide and the
 CC proteins may be used directly or indirectly, e.g. using antibodies to the
 CC proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's sarcoma,
 CC Castleman's disease, multiple myeloma and body cavity based large cell
 CC lymphoma (BCHL). The proteins have also been claimed to be useful in
 CC screening compounds for drugs to treat HHV-8 diseases.

XX Sequence 204 AA;

Query Match 100.0%; Score 103; DB 19; Length 204;

Best Local Similarity 100.0%; Pred. No. 3e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNETSCLKRIADGFEFE 19
 Db 87 gfnetsclickiadgffefe 105

RESULT 5

AAW23944
 ID AAW23944 standard; Protein; 204 AA.

XX AAW23944;

XX 30-JUN-1998 (first entry)

XX Human herpesvirus 8 Interleukin-6.

XX Interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
 KM antibody; diagnosis; treatment.

XX Human herpesvirus 8.

XX MO9803657-A1.

XX 29-JAN-1998.

XX 19-JUL-1996; 96MO-EP03199.

XX 19-JUL-1996; 96MO-EP03199.

XX (BEHW) BEHRING DIAGNOSTICS GMBH.

XX (UYNY) UNIV NEW YORK STATE.

XX Albrecht J, Fleckenstein B, Friedman-Kien A, Huang Y;

XX WPI: 1998-120781/11.

XX Viral interleukin-6 produced recombinantly from human herpes virus 8
 PT DNA - and related nucleic acid and antibodies, used for diagnosis
 PT and treatment of herpes 8 infection or related diseases, e.g. Kaposi
 PT sarcoma

XX Claim 2; Fig 2; 19pp; English.

XX The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
 CC can be used to detect antibodies and antibodies can be used to detect
 CC IL-6. This can be used for the diagnosis of HHV8 infection or
 CC associated diseases such as Kaposi sarcoma or kidney cell carcinoma.
 CC Antibodies, proteins and the gene sequence can all be used in the
 CC treatment of infections and diseases as mentioned above.

XX Sequence 204 AA;

Query Match 100.0%; Score 103; DB 19; Length 204;

Best Local Similarity 100.0%; Pred. No. 3e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GFNETSCLKRIADGFEFE 19
 Db 87 gfnetsclickiadgffefe 105

RESULT 6

AAW77391
 ID AAW77391 standard; Protein; 162 AA.

XX AAW77391;

XX 17-APR-1996 (first entry)

XX Human mutant IL-6a/C1 (amino acids 5-19 and 44-50 deleted).

XX Human interleukin-6; IL-6a/C1 mutant; increased stability;

XX recombinant; production; deletion mutant;

XX amino acids 5-19 and 44-50.

OS Homo sapiens.

XX JP07224097-A.
 XX
 XX 22-AUG-1995.
 XX
 XX 08-FEB-1994; 94JP-0014461.
 XX
 XX 08-FEB-1994; 94JP-0014461.
 XX
 XX (ASAG) ASahi GLASS CO LTD.
 XX
 XX WPI: 1995-325556/42.
 XX N-PSDB; AAQ94346.
 XX Interleukin-6 mutant, related DNA and expression vectors - has
 XX higher stability than natural Interleukin-6
 XX
 XX Claim 1: Page 14; 18pp; Japanese.
 XX
 XX AAQ94346 encodes AAR77391 the human IL-6 deletion mutant IL-6a'Cl,
 XX which lacks the amino acids Gly5-Leu19 and Cys44-Cys50 of the
 XX wild type protein. The cDNA can be used for the recombinant prodn.
 XX of IL-6a'Cl, which has increased stability compared to wild type
 XX IL-6.
 XX
 XX Sequence 162 AA:

Query Match 59.2%; Score 61; DB 16; Length 162;
 Best Local Similarity 57.9%; Pred. No. 0.018;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENEISCLKKLADGFFRE 19
 ||||| :||| :| |||
 Db 55 gineetclvklitglllefe 73

RESULT 7

AAW00131
 ID AAW00131 standard; Protein: 162 AA.

AC AAW00131;

DT 09-APR-1997 (first entry)

XX Human Interleukin-6 fragment.

XX Secretary: signal peptide; P-factor; multicloning vector; PCR;

XX animal protein; expression; production; recombinant; primer;

XX fission yeast; human; serum albumin; interleukin-6;

XX polymerase chain reaction; Schizosaccharomyces pombe;

XX Homo sapiens.

XX WO9623890-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASahi GLASS CO LTD.

XX Hama Y, Kumagai H, Nikaido K, Tohda H, Tsukamoto H;

XX WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene
 XX PT - for production of vectors for expression of animal proteins in a
 XX fission yeast, pref. S. pombe, host

PS Example 4; Pages 28-29; 50pp; Japanese.
 XX
 XX A multicloning vector, comprising the human interleukin-6 (hIL-6)
 XX cDNA, a Schizosaccharomyces pombe secretory signal peptide
 XX fragment or P-factor fragment (PO fragment) DNA and preferably an
 XX animal cell viral promoter sequence and a neomycin resistance gene,
 XX can be used for the efficient production of a hIL-6 fragment, i.e.
 XX the present sequence, in a fission yeast host, preferably S. pombe,
 XX culture.
 XX
 XX Sequence 162 AA:

Query Match 59.2%; Score 61; DB 17; Length 162;
 Best Local Similarity 57.9%; Pred. No. 0.018;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENEISCLKKLADGFFRE 19
 ||||| :||| :| |||
 Db 55 gineetclvklitglllefe 73

RESULT 8

AAW00132
 ID AAW00132 standard; Protein: 163 AA.

AC AAW00132;

DT 09-APR-1997 (first entry)

XX Human Interleukin-6 fragment.

XX Secretary: signal peptide; P-factor; multicloning vector; PCR;

XX animal protein; expression; production; recombinant; primer;

XX fission yeast; human; serum albumin; interleukin-6;

XX polymerase chain reaction; Schizosaccharomyces pombe;

XX Homo sapiens.

XX WO9623890-A1.

XX 08-AUG-1996.

XX 01-FEB-1996; 96WO-JP00198.

XX 03-FEB-1995; 95JP-0017167.

XX (ASAG) ASahi GLASS CO LTD.

XX Hama Y, Kumagai H, Nikaido K, Tohda H, Tsukamoto H;

XX WPI: 1996-371438/37.

XX Schizosaccharomyces pombe secretory signal peptide (P-factor) gene
 XX PT - for production of vectors for expression of animal proteins in a
 XX fission yeast, pref. S. pombe, host

XX Example 7; Pages 30-31; 50pp; Japanese.

XX A multicloning vector, comprising the human interleukin-6 (hIL-6)

XX cDNA, a Schizosaccharomyces pombe secretory signal peptide

XX fragment or P-factor fragment (PI fragment) DNA and preferably an

XX animal cell viral promoter sequence and a neomycin resistance gene,
 XX can be used for the efficient production of a hIL-6 fragment, i.e.
 XX the present sequence, in a fission yeast host, preferably S. pombe,
 XX culture.

XX Sequence 163 AA:

Query Match 59.2%; Score 61; DB 17; Length 163;
 Best Local Similarity 57.9%; Pred. No. 0.018;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFEFE 19
||||:||||:|
Db 56 gfineetclvklitgllefe 74

RESULT 9
AAR77649
ID AAR77649 standard; Protein: 167 AA.

AC AAR77649;

DT 27-JUN-1996 (first entry)

DE Human interleukin-6 splice variant.

KW Human: interleukin-6; splice variant; IL-6SV; treatment;

KW immunotherapy; anti-inflammatory; bone marrow transplant;

KW chemotherapy; side effect; corneal damage; keratitis; ulcer;

KW antagonist; Castleman's disease; multiple myeloma;

KW cardiac myxoma; cervical cancer; rheumatoid arthritis;

KW autoimmune diabetes; sepsis.

OS Homo sapiens.

PN WO9532282-A1.

PD 30-NOV-1995.

PF 17-MAY-1995; 95WO-US06094.

PR 19-MAY-1994; 94US-0246427.

PS (HUMA-) HUMAN GENOME SCI INC.

PI Adams MD, Li H, Ruben S;

DR WPI; 1996-020577/02.

DR N-PSDB; AAT08558.

PT Polynucleotide encoding Interleukin 6-splice variant - used for

PS Claim 1; Page 40; 54pp: English.

CC The human interleukin-6 splice variant (IL-6SV) AAR77649 is encoded

CC by AAT08558 (which is derived from an activated macrophage cDNA

CC library), and may be used in immunotherapeutic and

CC anti-inflammatory compounds, and for the treatment of patients

CC suffering from bone marrow transplant chemotherapy side effects,

CC corneal damage, keratitis and ulcers. Antagonists of IL-6SV may

CC be used to treat diseases caused by the up-regulated prodn. of

CC IL-6 (i.e. Castleman's disease, multiple myeloma, cardiac myxoma,

CC cervical cancer, rheumatoid arthritis and autoimmune diabetes),

CC and sepsis.

XX Sequence 167 AA;

SO

XX

AC AAR77387;
DT 17-APR-1996 (first entry)

DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).

KW Human interleukin-6; IL-6a mutant; increased stability;

KW recombinant; production; deletion mutant; amino acids 5-19.

OS Homo sapiens.

PN JP07224097-A.

PD 22-AUG-1995.

PF 08-FEB-1994; 94JP-0014461.

PR 08-FEB-1994; 94JP-0014461.

PA (ASAG) ASAHI GLASS CO LTD.

DR WPI; 1995-32556/42.

DR N-PSDB; AAQ94342.

PT Interleukin-6 mutant, related DNA and expression vectors - has

PS Claim 1; Page 10; 18pp: Japanese.

CC AAQ94342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which

CC lacks the amino acids G15-Len19 of the wild type protein. The

CC cDNA can be used for the recombinant prodn. of IL-6a, which has

SO increased stability compared to wild type IL-6.

Sequence 169 AA;

Query Match 59.2%; Score 61; DB 16; Length 169;

Best Local Similarity 57.9%; Pred. No. 0.019;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFEFE 19
||||:||||:|
Db 62 gfineetclvklitgllefe 80

RESULT 11
AAR75342
ID AAR75342 standard; Protein: 174 AA.

AC AAR75342;

DT 13-DEC-1995 (first entry)

DE Hybrid human cytokine IIIL.

KW Hybrid cytokine; tumour proliferation; cancer therapy.

OS Synthetic.

PN Key Location/Qualifiers

PD Misc-difference 173

PF MISC-difference 173

PR 07-NOV-1994; 94WO-US12873.

PR 08-NOV-1993; 93US-0149101.

PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

CC AA094343 encodes AAR7388 the human IL-6 deletion mutant IL-6c1,
 CC which lacks the amino acids Cys44-Cys50 of the wild type protein.
 CC The cDNA can be used for the recombinant prodn. of IL-6c1, which
 CC has increased stability compared to wild type IL-6.
 CC XX
 SQ Sequence 177 AA;

Query Match 59.2%; Score 61; DB 16; Length 177;
 Best Local Similarity 57.9%; Pred. No. 0.02;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19
 ||||:||||:|
 Db 70 gfnecclvklitgllfe 88

RESULT 14

AAR75334
 ID AAR75334 standard; Protein: 179 AA.

XX AAR75334;
 AC AAR75334;

XX 13-DEC-1995 (first entry)
 DT 13-DEC-1995 (first entry)

XX Human interleukin-6 (IL-6).
 DE Human interleukin-6 (IL-6).

XX Cytokine; tumour proliferation; cancer therapy.
 KM Cytokine; tumour proliferation; cancer therapy.

XX Homo sapiens.
 OS Homo sapiens.

XX WO9513393-A.
 PN WO9513393-A.

XX 18-MAY-1995.
 PD 18-MAY-1995.

XX 07-NOV-1994; 94WO-US12873.
 PF 07-NOV-1994; 94WO-US12873.

XX 08-NOV-1993; 93US-0149101.
 PR 08-NOV-1993; 93US-0149101.

XX (HUTC-) HUTCHINSON CANCER RES CENTER FRED.
 PA (HUTC-) HUTCHINSON CANCER RES CENTER FRED.

XX Leung DW, Rose TM, Todaro GJ;
 PI Leung DW, Rose TM, Todaro GJ;

XX WPI; 1995-194111/25.
 DR WPI; 1995-194111/25.

XX N-PSDB; AA087153.
 DR N-PSDB; AA087153.

XX New hybrid cytokines with alpha helical sequences from different
 PT sources - also DNA encoding them, vectors and transformed cells,
 PT useful e.g. for treating cancer, remodelling bone etc.
 PT useful e.g. for treating cancer, remodelling bone etc.

XX Disclosure; Page 23-24; 52pp; English.
 PS Disclosure; Page 23-24; 52pp; English.

XX The cytokine encoding genes for leukemia inhibitory factor (LIF),
 CC granulocyte-colony stimulating factor (G-CSF), interleukin-6 (IL-6),
 CC interleukin-11 (IL-11), ciliary neurotrophic factor (CNTF) and
 CC oncostatin-M (OSM) have been cloned and reported in the literature.
 CC IL-6, G-CSF, LIF, IL-11, CNTF and OSM each comprise four alpha-
 CC helical sequences. In each cytokine, the four alpha-helical
 CC sequences are linked by non-alpha-helical 'linking' sequences of
 CC about 5-100 AAs; and in some cases the alpha-helices are maintained
 CC in the proper conformation and geometry with respect to each other
 CC through disulfide bridges. The invention provides a group of
 CC therapeutic hybrid cytokines, having a size ranging from about 10
 CC to about 30 kDa. Each hybrid cytokine comprises three or four
 CC alpha-helical sequences and linking sequences, ranging from about
 CC 5-40 AAs in length, selected from the linking sequences of the
 CC above cytokines or other linking sequences.
 CC above cytokines or other linking sequences.
 CC above cytokines or other linking sequences.
 XX Sequence 179 AA;

Query Match 59.2%; Score 61; DB 16; Length 179;
 Best Local Similarity 57.9%; Pred. No. 0.02;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GFNETSCLKRLADGFFFE 19
 ||||:||||:|
 Db 72 gfnecclvklitgllfe 90

RESULT 15

AAR60125
 ID AAR60125 standard; Protein: 183 AA.

XX AAR60125;
 AC AAR60125;

XX 21-MAR-1995 (first entry)
 DT 21-MAR-1995 (first entry)

XX Human interleukin 6 (IL-6).
 DE Human interleukin 6 (IL-6).

XX Interleukin; IL-6; chromatography; purification; isolation.
 KM Interleukin; IL-6; chromatography; purification; isolation.

XX Homo sapiens.
 OS Homo sapiens.

XX US5338834-A.
 PN US5338834-A.

XX 16-AUG-1994.
 PD 16-AUG-1994.

XX 26-JAN-1993; 93US-0009973.
 PF 26-JAN-1993; 93US-0009973.

XX 26-JAN-1993; 93US-0009973.
 PR 26-JAN-1993; 93US-0009973.

XX (ALLX) ALLELIX BIOPHARMACEUTICALS INC.
 PA (ALLX) ALLELIX BIOPHARMACEUTICALS INC.

XX Williams AM;
 PI Williams AM;

XX WPI; 1994-263330/32.
 DR WPI; 1994-263330/32.

XX N-PSDB; AA070446.
 DR N-PSDB; AA070446.

XX Method for obtaining pure human interleukin-6 - comprises 3-step
 PT purification method using chromatography techniques
 PT purification method using chromatography techniques

XX Disclosure; Figure 1; 13pp; English.
 PS Disclosure; Figure 1; 13pp; English.

XX A method for obtaining pure interleukin-6 (IL-6) comprises (a)
 CC fractionating a preparation containing human IL-6 by cation-exchange
 CC chromatography using a column comprising a cationic resin and
 CC eluting a first IL-6 sample; (b) fractionating the first IL-6 sample
 CC by hydrophobic chromatography using a column comprising a
 CC hydrophobic adsorbent and eluting from the column a second IL-6
 CC sample; (c) fractionating the second IL-6 sample by reverse phase
 CC HPLC in the presence of a cationic charge modifier; and (d)
 CC collecting pure IL-6. (Steps (a) and (b) are interchangeable). The
 CC obtained IL-6 has a purity of >98%.
 CC obtained IL-6 has a purity of >98%.
 XX Sequence 183 AA;

SQ Sequence 183 AA;

Query Match 59.2%; Score 61; DB 15; Length 183;
 Best Local Similarity 57.9%; Pred. No. 0.02;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19
 ||||:||||:|
 Db 76 gfnecclvklitgllfe 94

Search completed: October 4, 2001, 18:52:08
 Job time: 1674 sec.

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:51 ; Search time 44.98 Seconds
(without alignments)
32.177 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105
Perfect score: 103
Sequence: 1 GENETSCUKKLADGFEFEFE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues
Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_68:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	61	59.2	212	1	IVHUB2
2	55	53.4	208	2	T09216
3	53	51.5	212	2	I46621
4	53	51.5	212	2	I46580
5	51	49.5	207	2	I46084
6	49	47.6	211	2	A34247
7	48	46.6	162	2	H83786
8	47	45.6	211	1	ICMS6
9	47	45.6	745	2	T05375
10	46	44.7	208	1	S29549
11	46	44.7	568	2	C82379
12	45	43.7	484	2	F71061
13	44	42.7	282	2	D70149
14	44	42.7	454	2	T27249
15	44	42.7	1893	2	T22661
16	44	42.7	2875	1	RRVUTW
17	44	42.7	4196	2	T43274
18	43	41.7	157	2	H69203
19	43	41.7	208	1	A56610
20	43	41.7	231	2	H83664
21	42.5	41.3	492	2	T30066
22	42	40.8	180	2	H72402
23	42	40.8	364	2	T23819
24	42	40.8	512	2	S47900
25	42	40.8	861	2	T41945
26	42	40.8	1690	2	T13030
27	42	40.8	2048	1	ZLNZSE
28	42	40.8	2139	2	S46404
29	42	40.8	2228	1	ZLNZSV

30	42	40.8	2233	1	ZLNZP3	genome polypotein
31	41.5	40.3	386	2	E81443	hypothetical prote
32	41	39.8	158	2	T17748	hypothetical prote
33	41	39.8	159	1	E11208	hypothetical prote
34	41	39.8	320	2	S22615	hypothetical prote
35	41	39.8	343	2	JM0249	vancomycin resista
36	41	39.8	669	2	T51220	hypothetical prote
37	41	39.8	787	2	T00798	hypothetical prote
38	41	39.8	1224	2	S25952	gene cob Inturon 3
39	41	39.8	1642	2	T08880	NMDA receptor-bind
40	40.5	39.3	244	2	JC2425	glutathione transf
41	40.5	39.3	695	2	T28782	hypothetical prote
42	40.5	39.3	1276	2	S75801	probable phytochro
43	40	38.8	88	2	A48595	major allergen lo1
44	40	38.8	97	2	A44291	pollen allergen lo
45	40	38.8	152	2	B64485	hypothetical prote

ALIGNMENTS

RESULT 1
IVHUB2
Interleukin-6 precursor [validated] - human
N: Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C: Species: Homo sapiens (man)
C: Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 08-Dec-2000
C: Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601;
R: Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A: Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) g
A: Accession: A32648; MUID:88082664
A: Reference number: A32648; MUID:88082664
A: Molecule type: DNA
A: Residues: 1-212 <YAS>
A: Cross-references: GB:Y00081; NID:929494; PIDN:CA468278.1; PID:929495
A: Note: the authors translated the codon CAG for residue 130 as Glu
R: Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A: Title: Structure and expression of cDNA and genes for human Interferon-beta-2, a dI
A: Reference number: A91051; MUID:87053818
A: Accession: A25692
A: Molecule type: mRNA
A: Residues: 1-212 <ZIL>
A: Cross-references: GB:X04430; NID:932673; PIDN:CA428026.1; PID:932674
R: Hirano, T.; Yasukawa, K.; Harada, H.; Iaga, T.; Watanabe, Y.; Matsuda, T.; Kashim
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A: Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymph
A: Reference number: A93387; MUID:87065033
A: Accession: A26966
A: Molecule type: mRNA
A: Residues: 1-212 <HIR>
A: Cross-references: GB:X04602; NID:933849; PIDN:CA428268.1; PID:933850
R: Tounouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A: Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A: Reference number: A33515; MUID:89391958
A: Accession: A33515
A: Molecule type: mRNA
A: Residues: 1-212 <TON>
A: Cross-references: GB:M29150; NID:9166349; PIDN:AA59154.1; PID:9307063
R: Haegeman, G.; Content, J.; Voelckert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A: Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A: Reference number: A25801; MUID:87004683
A: Accession: A25801
A: Molecule type: DNA; mRNA
A: Residues: 1-212 <HAE>
A: Cross-references: GB:X04403
A: Experimental source: Fibroblast
R: May, L.T.; Heligott, D.C.; Sehgal, P.B.

Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-Interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; M0ID:87067453
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAX>
 A:Cross-references: GB:M14584; NID:q184628; PIDN:AAA52728.1; PID:q306910
 R:Mong, G.C.; Wilck-Glenneff, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Behring Inst. Mtt. 83, 40-47, 1988
 A>Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: 152193; M0ID:89193317
 A:Accession: 152193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:q186351; PIDN:AA41704.1; PID:q186352
 R:Krenkel, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
 A:Reference number: 156003; M0ID:88088768
 A:Accession: 156003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212

 A:Cross-references: GB:M18403; NID:q184631; PIDN:AA52729.1; PID:q306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor
 A:Reference number: A92816; M0ID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', '53-57', 'X', '59', 'X', '61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', '59-61', 'X', '63 <VA2>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; M0ID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hirano, T.; Tada, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; M0ID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Node, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; An Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiation
 A:Reference number: A61159; M0ID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <MOD>
 A:Experimental source: fibroblast
 R:Ming, J.E.; Cernetti, C.; Steiman, R.M.; Graneli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytokine T lymphocyte differentiation factor for
 A:Reference number: A61462; M0ID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zabitsky, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Reference number: A48419; M0ID:91355844
 A:Accession: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', '39-40 <MAX2>
 A:Experimental source: FS-4 fibroblasts

A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30K form contained both N-linked and O-linked carbohydrate; a 25K for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAX3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBI:63787)
 A>Note: this 23-25K form contained O-linked but not N-linked carbohydrate
 R:Ortiz, T.; Oheba, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; M0ID:9426765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clogston, C.L.; Boone, T.C.; Grandell, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; M0ID:89261115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ide, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; M0ID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:116
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/Domain: signal sequence #status predicted <Sig>
 F:28-212/Product: interleukin-6, long form #status experimental <NATL>
 F:30-212/Product: interleukin-6, short form #status experimental <NATL>
 F:72-78, 101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.2%; Score 61; DB 1; Length 212;
 Best Local Similarity 57.9%; Pred. No. 0.016;
 Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLKRLADGFFEE 19
 DB 105 GFNEBCLVKTITGLLEFE 123

RESULT 2
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C>Date: 11-Jun-1999 #sequence #revision 11-Jun-1999 #text change 23-Jul-1999
 C:Accession: T09216
 R:Swiderski, C.E.; Horohov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: Z16613
 A:Accession: T09216
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-208 <SMI>
 A:Cross-references: EMBL:U64794; NID:92654387; PID:92654388
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: interleukin-6
 C:Keywords: cytokine; growth factor

Query Match 53.4%; Score 55; DB 2; Length 208;
 Best Local Similarity 47.4%; Pred. No. 0.15;

Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKRLADGFFEE 19
|||:||||:|
Db 102 GFNETCICMRITTTGLSEFO 120

RESULT 3
146621
Prointerleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146621
R:Richards, C.; Saklatva, J.
Cytokine 3, 269-276, 1991
A:Title: Molecular Cloning and Sequence of Porcine Interleukin 6 cDNA and Expression of
A:Reference number: 146621; MUID:91338547
A:Accession: 146621
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <R1C>
A:Cross-references: GB:M86722; NID:g164624; PIDN:ANC3733.1; PID:g164625
C:Genetics:
A:Gene: IL6
C:Superfamily: Interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.33;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKRLADGFFEE 19
|||:||||:|
Db 105 GFNETCICMRITTTGLSEFO 123

RESULT 4
146590
Interleukin 6 - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
C:Accession: 146590
R:Mathalagan, N.; Bixby, J.; Roberts, M.R.
Mol. Reprod. Dev. 32, 324-330, 1992
A:Title: Expression of Interleukin-6 in porcine, ovine, and bovine preimplantation conce
A:Reference number: 146590; MUID:92360284
A:Accession: 146590
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-212 <MAT>
A:Cross-references: GB:M80258; NID:g164514; PIDN:ANC27127.1; PID:g164515
C:Genetics:
A:Gene: IL-6
C:Superfamily: Interleukin-6

Query Match 51.5%; Score 53; DB 2; Length 212;
Best Local Similarity 42.1%; Pred. No. 0.33;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKRLADGFFEE 19
|||:||||:|
Db 105 GFNETCICMRITTTGLSEFO 123

RESULT 5
146084
Interleukin 6 - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: 146084
R:Bradley, W.G.; Gibbs, C.; Kraus, L.; Good, R.A.; Day, N.K.
Proc. Soc. Exp. Biol. Med. 204, 301-305, 1993

A:Title: Molecular cloning and characterization of a cDNA encoding feline Interleukin
A:Reference number: 146084; MUID:94052249
A:Accession: 146084
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-207 <BRA>
A:Cross-references: GB:L16914; NID:g438519; PIDN:AAA16620.1; PID:g438520
C:Superfamily: Interleukin-6

Query Match 49.5%; Score 51; DB 2; Length 207;
Best Local Similarity 42.1%; Pred. No. 0.69;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 GFNETSCLKRLADGFFEE 19
|||:||||:|
Db 101 GFNETCICMRITTTGLSEFO 119

RESULT 6
A34247
Interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northemann, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-der
A:Reference number: A34247; MUID:9380206
A:Accession: A34247
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NOR>
A:Cross-references: GB:M26744; NID:g204915; PIDN:AAA7659.1; PID:g204916
C:Superfamily: Interleukin-6
C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 47.6%; Score 49; DB 2; Length 211;
Best Local Similarity 44.4%; Pred. No. 1.5;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 1 GFNETSCLKRLADGFFEE 18
|||:||||:|
Db 103 GYNOEICLKIKCSGLER 120

RESULT 7
H83786
Hypothetical protein BH1096 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C:Accession: H83786
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: A83650; MUID:20263314
A:Accession: H83786
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <STO>
A:Cross-references: GB:AF001510; GB:BA000004; NID:g10173440; PIDN:BAB04815.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1096

Query Match 46.6%; Score 48; DB 2; Length 162;
Best Local Similarity 66.7%; Pred. No. 1.7;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 5 TSCIKRLADGFFEE 19

```

DB      31 TSMIEIGADGFFEF 45
RESULT  8
ICMS6
Interleukin-6 precursor - mouse
N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatocytoma growth factor
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence, revision 30-Jun-1990 #text, change 22-Jun-1999
C:Accession: A30531; A27610; A30571; S01323; E34047; A26662; A40486; A60799; S10
R:Rabin, O.; Akita, S.; Kamiya, T.; Wong, G.C.; Hirano, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A>Title: Genomic structure of the murine IL-6 gene. High degree conservation of potential
A:Reference number: A30531; MUID:89035525
A:Accession: A30531
A:Molecule type: DNA
A:Residues: 1-211 <TRAN>
A:Cross-references: GB:M20572; NID:9198369; PIDN:AAA39302.1; PID:9387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renauld, J.C.; Van Roost, E.; Boon, T.; Sim
Eur. J. Immunol. 18, 193-197, 1988
A>Title: cDNA cloning of murine Interleukin-6: homology with human Interleukin 6.
A:Reference number: A27610; MUID:88166883
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <VAN>
A:Cross-references: GB:X06203; NID:952701; PIDN:CAA29560.1; PID:952702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cle
J. Immunol. 142, 1372-1376, 1989
A>Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MOC>
A:Cross-references: NID:M24221; NID:9341131; PIDN:AAA68814.1; PID:9870699
R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A>Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and
A:Reference number: S01323; MUID:88329059
A:Accession: S01323
A:Molecule type: protein
A:Residues: 25-166 'X', 168-211 <SIM>
A>Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
R:Grenet, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A>Title: Cloning and sequence analysis of the cDNA for murine Interleukin-6.
A:Reference number: S12103; MUID:91057159
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <GRE>
A:Cross-references: EMBL:X54542; NID:952727; PIDN:CAA38411.1; PID:952728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A>Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69 'X', 71-75; 78-94; 128-148 <JAS>
R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoe, C.; Coulle, P.G.; Rubira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A>Title: Multiple biological activities are expressed by a mouse Interleukin 6 cDNA clon
A:Reference number: A40486; MUID:89017145
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>

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```

A:Cross-references: GB:J03783; NID:9198367; PIDN:AAA39301.1; PID:9309410
R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.
Blood 72, 2070-2073, 1988
A>Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin
A:Reference number: A60799; MUID:89062753
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A>Title: DNA rearrangement and constitutive expression of the Interleukin 6 gene in a
A:Reference number: S10241; MUID:90171860
A:Accession: S10241
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:949738; PIDN:CAA35824.1; PID:9581860
R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 217, 53-59, 1993
A>Title: Specific covalent modification of the tryptophan residues in murine Interleu
A:Reference number: S38254; MUID:94039075
A:Accession: S38254
A>Status: preliminary
A:Molecule type: protein
A:Residues: 38-60; 75, 'X', 77-79; 176-203 <ZHA>
C:Genetics:
A:Gene: 11-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: Interleukin-6
C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine
F:1-24/Domain: signal sequence *status predicted <SIG>
F:25-211/Product: Interleukin-6 *status experimental <MNT>

```

```

Query Match          45 68; Score 47; DB 1; Length 211;
Best Local Similarity 38.98; Pred. No. 3.2;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

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DB      103 GYNEICLKLKISSGLE 120

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RESULT  9
T05375
hypothetical protein F16G20.70 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence, revision 23-Apr-1999 #text, change 23-Jul-1999
C:Accession: T05375
R:Bevan, M.; Watson, M.D.; Gibbons, T.; Bartley, J.; Bancroft, I.; Mewes, H.W.; Mayer
submitted to the Protein Sequence Database, August 1998
A:Reference number: Z15413
A:Accession: T05375
A:Molecule type: DNA
A:Residues: 1-745 <BEV>
A:Cross-references: EMBL:AL031326
A:Experimental source: cultivar Columbia; BAC clone F16G20
C:Genetics:
A:Map position: 4
A:Introns: 22/2; 121/1; 159/3; 234/3; 286/3; 366/3; 450/1; 490/3; 519/3; 572/3; 620/3
A>Note: F16G20.70

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Query Match          45 68; Score 47; DB 2; Length 745;
Best Local Similarity 47.18; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

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DB      289 GFNKTGCVNLCRGFVG 305

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RESULT 10
S29549
Interleukin-6 - sheep
C:Species: Ovis orientalis arles, Ovis ammon arles (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29549
R:Ebrahim, B.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29549
A:Accession: S29549
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <EBR>
A:Cross-references: EMBL:X68723
C:Superfamily: Interleukin-6

Query Match 44.7%; Score 46; DB 1; Length 208;
Best Local Similarity 42.1%; Pred. No. 4.6;
Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 GENETSCCLKADGFFEE 19
||| ||| ||| |||
Db 105 GFNQAVCLIKTTAGLELYQ 123

RESULT 11
C82379
response regulator VCA1086 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: C82379
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.T.;
charlson, D.; Esmolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Drygol, I.; Sellers, F.
l, R.R.; Mekalanos, J.T.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833
A:Accession: C82379
A:Molecule type: DNA
A>Status: preliminary
A:Residues: 1-568 <HEI>
A:Cross-references: GB:AE004434; GB:AE003853; NID:g9658531; PIDN:AFP6979.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA1086
A:Map position: 2

Query Match 44.7%; Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 SCLKTLADGFFEE 18
||| ||| ||| |||
Db 460 SSLKETPDGFFEE 472

RESULT 12
F71061
hypothetical protein PH188 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 18-Aug-2000
C:Accession: F71061
R:Kawarabayashi, Y.; Sasaki, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Seki,
M.; Onikubo, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushi, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: F71061
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-484 <KAW>

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A:Cross-references: GB:AP000005; NID:g3236132; PIDN:BAA30288.1; PID:d1031231; PID:g32
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by Genba
C:Genetics:
A:Gene: PH1188
C:Superfamily: Pyrococcus horikoshii hypothetical protein PH1188

Query Match          43.7%; Score 45; DB 2; Length 484;
Best Local Similarity 33.3%; Pred. No. 15;
Matches 6; Conservative 8; Mismatches 4; Indels 0; Gaps 0;

OY      1  GNETSCLKLADGFEFF 18
      1 : 11 : 11 : 11 :
DB      75  GYGKTSIMRALAEGIYD 92

RESULT 13
D70149
hypothetical protein BB0397 - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: D70149
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wh
son, D.; Peterson, J.; Kertavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vu
Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:96065943
A:Accession: D70149
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-282 <KLE>
A:Cross-references: GB:AE001145; GB:AE000783; NID:z2688296; PIDN:AC66779.1; PID:g2686
A:Experimental source: strain B51

Query Match          42.7%; Score 44; DB 2; Length 282;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY      2  FNETSCLKLADGFF 16
      1 : 11 111 11 11
DB     177  YNNTSGSKKLEDSFF 191

RESULT 14
T27249
hypothetical protein Y5F2A.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27249
R:Lenhard, N.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20331
A:Accession: T27249
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-454 <WLL>
A:Cross-references: EMBL:AL032641; PIDN:CAA21647.1; GSPDB:GN00022; CESP:Y5F2A.4
A:Experimental source: clone Y5F2A
C:Genetics:
A:Gene: CESP:Y5F2A.4
A:Map position: 4
A:introns: 17/2; 50/3; 125/3; 159/3; 201/3; 241/2; 353/1; 411/1

Query Match          42.7%; Score 44; DB 2; Length 454;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 10; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

OY      3  NETSCLKLKLA-----DGFF 16

```

DB 177 HETSLKRFAPVCKPDDSTF 196

RESULT 15

T22661 hypothetical protein T01G1.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C:Accession: T22661; T24305

R:White, S.; Morlmore, B. submitted to the EMBL Data Library, November 1996

A:Reference number: 219594

A:Accession: T22661

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1893 <WIL>

A:Cross-references: EMBL:Z82271; PIDD:CA805214.1; GSPDB:GNO0022; CESP:T01G1.1

A:Experimental source: clone F54E12

R:Kirschner, J.

submitted to the EMBL Data Library, March 1997

A:Reference number: 219872

A:Accession: T24305

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1893 <W12>

A:Cross-references: EMBL:Z92811; PIDD:CA807273.1; GSPDB:GNO0022; CESP:T01G1.1

A:Experimental source: clone T01G1

C:Genetics:

A:Gene: CESP:T01G1.1

A:Map position: 4

A:Introns: 65/3; 101/3; 194/3; 269/3; 299/2; 373/3; 481/3; 576/3; 615/2; 704/3; 839/1; 9

Query Match

42.7%; Score 44; DB 2; Length 1893;

Best Local Similarity 58.3%; Pred. No. 87;

Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 6 SCLKRLADGFFE 17

DB 351 SCVEKLVGDLFD 362

Search completed: October 4, 2001, 19:09:53
Job time: 1254 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:12:31 ; Search time 27.34 Seconds
(without alignments)
23.806 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105
Perfect score: 103
Sequence: 1 GENETSCIKLADGFFEE 19

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues
Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	59.2	212	1	IL6_CERTO
2	61	59.2	212	1	IL6_HUMAN
3	61	59.2	212	1	IL6_MACRA
4	61	59.2	212	1	IL6_MACMU
5	55	53.4	208	1	IL6_HORSE
6	54	52.4	209	1	IL6_HOVI
7	53	51.5	207	1	IL6_CANFA
8	53	51.5	212	1	IL6_PIG
9	51	49.5	205	1	IL6_ORCOR
10	51	49.5	208	1	IL6_FELCA
11	49	47.6	211	1	IL6_RAT
12	48	46.6	207	1	IL6_MARMO
13	47	45.6	201	1	IL6_MOUSE
14	46	44.7	208	1	IL6_CAPRI
15	46	44.7	208	1	IL6_SHEEP
16	44	42.7	2875	1	RRPL_TSMV1
17	44	42.7	4196	1	DYHC_SCHPO
18	43	41.7	125	1	IL6_MUSVI
19	43	41.7	208	1	IL6_HOVI
20	42	40.8	512	1	RCK1_YEAST
21	42	40.8	861	1	UL52_HSV7J
22	42	40.8	2048	1	RRPL_SENDE
23	42	40.8	2148	1	VITL_AEDAE
24	42	40.8	2228	1	RRPL_SENDS
25	42	40.8	2228	1	RRPL_SENDF
26	42	40.8	2228	1	RRPL_SENDE
27	42	40.8	2233	1	RRPL_SENDE
28	41	39.8	343	1	VANC_P13H4
29	40.5	39.3	243	1	GTT2_RAT
30	40.5	39.3	559	1	PHF1_MOUSE
31	40.5	39.3	567	1	PHF1_HUMAN
32	40.5	39.3	1276	1	PHY2_STY3
33	40	38.8	97	1	MPL2_LOLPR

34	40	38.8	152	1	YEB3_METUA
35	40	38.8	258	1	PCNA_YEAST
36	40	38.8	348	1	GALM_STRTR
37	39.5	38.3	134	1	LEGI_BOVIN
38	39.5	38.3	134	1	LEGI_SHEEP
39	39.5	38.3	134	1	RRPL_THOGV
40	39	37.9	93	1	IM10_YEAST
41	39	37.9	252	1	PMW_CANAL
42	39	37.9	359	1	ALF1_RHOSH
43	39	37.9	378	1	UL25_HSV6G
44	39	37.9	553	1	NOEB_RHIME
45	39	37.9	555	1	UL25_HSV6U

ALIGNMENTS

```

RESULT 1
ID IL6_CERTO STANDARD; PRT; 212 AA.
AC P46650;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-PUI;
RX MEDLINE=36003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT *Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.*;
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL; L26032; AAA99972.1; -.
DR HSSP; P05231; IALU.
DR InterPro; IPR001716; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GSEMGF.
DR PROSITE; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29
FT CHAIN 30 212
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT CARBOHYD 172 172
SQ SEQUENCE 212 AA; 23668 MW; C73C035226B449BF CRC64;

```

Query Match 59.2%; Score 61; DB 1; Length 212;
Best Local Similarity 57.9%; Pred. No. 0.0049;

Matches	11: Conservative	2: Mismatches	6: Indels	0: Gaps
Oy	1 GNETSCIKLADGFEPE 19			
Db	105 GNETDCLAKITGLTLEFE 123			
	: :			
RESULT 2				
IL6_HUMAN				
ID	IL6_HUMAN	STANDARD:	PRT:	212 AA.
AC	P05231.			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)			
DE	INTERFERON BETA-2) (HHRIDOMA GROWTH FACTOR).			
CN	IL6 OR IFNB2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid:9606;			
RN	11			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE-87065033; Pubmed-3491322;			
RA	Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,			
RA	Kashiwamura S.-I., Nakakima K., Koyama K., Iwanatsu A., Tsunashima S.,			
RA	Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;			
RT	*Complementary DNA for a novel human interleukin (BSF-2) that induces			
RL	B lymphocytes to produce immunoglobulin.*;			
RL	Nature 324:73-76(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-88082664; Pubmed-3500852;			
RA	Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,			
RA	Nakai S., Kishimoto T.;			
RT	*Structure and expression of human B cell stimulatory factor-2			
RL	(BSF-2/IL-6) gene.*;			
RL	EMBO J. 6:2939-2945(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-87067433; Pubmed-3538015;			
RA	May L.T., Helfgott D.C., Sehgal P.B.;			
RT	*Anti-beta-2 interferon antibodies inhibit the increased expression of			
RT	HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:			
RL	structural studies of the beta 2 interferon involved.*;			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-87053818; Pubmed-3023045;			
RA	Zilberstein A., Ruggieri R., Korn J.H., Revel M.;			
RT	*Structure and expression of cDNA and genes for human			
RT	interferon-beta-2, a distinct species inducible by growth-stimulatory			
RL	cytokines.*;			
RL	EMBO J. 5:2529-2537(1986).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-88088768; Pubmed-3320204;			
RA	Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,			
RA	Aarden L.A.;			
RT	*Molecular cloning and expression of hybridoma growth factor in			
RT	Escherichia coli.*;			
RL	J. Immunol. 139:4116-4121(1987).			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-89391958; Pubmed-2789513;			
RA	Tonouchi N., Miya K., Karasuyama H., Matsui H.;			
RT	*Deletion of 3' untranslated region of human BSF-2 mRNA causes			
RT	stabilization of the mRNA and high-level expression in mouse NIH3T3			
RL	cells.*;			
RL	Biochem. Biophys. Res. Commun. 163:1056-1062(1989).			
RN	[7]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE-Fibroblast;			


```

RL EMO J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X04430: CAA28026.1; -
DR EMBL: M14584: AAA52728.1; -
DR EMBL: X04602: CAA28268.1; -
DR EMBL: Y00081: CAA68278.1; -
DR EMBL: M18403: AAA52729.1; -
DR EMBL: M29150: AAA59154.1; -
DR EMBL: X04403: CAA27990.1; -
DR EMBL: X04403: CAA27991.1; -
DR EMBL: M54894: AAC41704.1; -
DR EMBL: S56892: AAD13886.1; -
DR EMBL: A09363: CAA00839.1; -
DR PIR: A32648: IVHUB2.
DR PIR: A25921: A25921.
DR PDB: 11L6: 04-FEB-98.
DR PDB: 21L6: 04-FEB-98.
DR PDB: 1AL0: 03-JUN-98.
DR MIM: 147620: -.
DR InterPro: IPR001716: -.
DR Pfam: PF00489: IL6.1.
DR PRINTS: PR00433: IL6GCSFMGF.
DR PRINTS: PR00434: INTERLEUKIN_6.1.
DR PROSITE: PS00254: INTERLEUKIN_6.1.
KM Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .).
FT MUTAGEN 173 173 A->V: ALMOST NO LOSS OF ACTIVITY.
FT MUTAGEN 185 185 W->R: NO LOSS OF ACTIVITY.
FT MUTAGEN 204 204 S->P: 13% ACTIVITY.
FT MUTAGEN 210 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
SQ SEQUENCE 212 AA; 23718 MW; 1F1ED1FE1B734079 CRC64;

Query Match 59.28; Score 61; DB 1; Length 212;
Best Local Similarity 57.96; Pred. No. 0.0049;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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QY 1 GFNETSCLIKLADGFEFE 19
ID 11111111111111111111
Db 105 GFNETSCLIKLADGFEFE 123

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RESULT 3
IL6_MACFA STANDARD; PRT; 212 AA.
AC P79341;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL: AB000554: BAA19148.1; -
DR HSSP: P05231: 21L6.
DR InterPro: IPR001716: -.
DR Pfam: PF00489: IL6.1.
DR PRINTS: PR00433: IL6GCSFMGF.
DR PRINTS: PR00434: INTERLEUKIN_6.
DR PROSITE: PS00254: INTERLEUKIN_6.1.
KM Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29
FT CHAIN 30 212 BY SIMILARITY.
FT DISULFID 72 78 INTERLEUKIN-6.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

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Query Match 59.28; Score 61; DB 1; Length 212;
Best Local Similarity 57.96; Pred. No. 0.0049;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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QY 1 GFNETSCLIKLADGFEFE 19
ID 11111111111111111111
Db 105 GFNETSCLIKLADGFEFE 123

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RESULT 4
IL6_MACMU STANDARD; PRT; 212 AA.
ID 11111111111111111111
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_Taxid=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RAC 2;
RX MEDLINE=96003435; Pubmed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN

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CC -----

DR EMBL: I46802; AAB01430.1; -

DR HSSP: P05231; 2IL6.

DR InterPro: IPR001716; -

DR Pfam: PF004489; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT NON_TER 1 1 BY SIMILARITY.

FT SIGNAL <1 26 INTERLEUKIN-6.

FT CHAIN 27 209 BY SIMILARITY.

FT DISULFID 69 75 BY SIMILARITY.

FT DISULFID 98 108 BY SIMILARITY.

SEQUENCE 209 AA; 23483 MW; 75144922E43B48E9 CRC64;

Query Match 52.4%; Score 54; DB 1; Length 209;

Best Local Similarity 42.1%; Pred. No. 0.071;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

DB 102 GFNETCLTRITGLLEFQ 120

QY 1 GFNETCLTKLADGFEFE 19

||||:||||:|

RESULT 7

IL6_CANFA STANDARD; PRT; 207 AA.

ID IL6_CANFA

AC PA1323;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_Taxid=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MONGREL;

RX MEDLINE=94303924; PubMed=7913298;

RA Michaela G.L., Youker K.A., Hawkins H.K., Perrard J.L.,

RA Michael H., Ballantyne C.M., Smith C.W., Entman M.L.;

RT "Regulation of ICM-1 and IL-6 in myocardial ischemia: effect of

RT reperfusion";

RL Ann. N.Y. Acad. Sci. 723:258-270(1994).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----

DR EMBL: U12234; AAA83030.1; -

DR HSSP: P05231; 2IL6.

DR InterPro: IPR001716; -

DR Pfam: PF004489; IL6; 1.

DR PRINTS: PR00433; IL6CSFMGF.

DR PRINTS: PR00434; INTERLEUKIN_6.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 26 POTENTIAL.

FT CHAIN 27 207 INTERLEUKIN-6.

FT DISULFID 67 73 BY SIMILARITY.

FT DISULFID 96 106 BY SIMILARITY.

SEQUENCE 207 AA; 22945 MW; 45540154EAC0F50 CRC64;

Query Match 51.5%; Score 53; DB 1; Length 207;

Best Local Similarity 42.1%; Pred. No. 0.1;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

DB 100 GFNETCLTRITGLVEFQ 118

QY 1 GFNETCLTKLADGFEFE 19

||||:||||:|

RESULT 8

IL6_PIG STANDARD; PRT; 212 AA.

ID IL6_PIG

AC P26893;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE INTERLEUKIN-6 PRECURSOR (IL-6).

GN IL6.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_Taxid=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=9138547; PubMed=1873476;

RA Richards C., Saklatvala J.;

RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and

RT expression of mRNA in synovial fibroblasts in vitro";

RL Cytokine 3:269-276(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=92360284; PubMed=1497880;

RA Mathalagan N., Bixby J.A., Roberts M.R.;

RT "Expression of interleukin-6 in porcine, ovine, and bovine

RT preimplantation conceptuses";

RL Mol. Reprod. Dev. 32:324-330(1992).

CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION

CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND

CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN

CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----

DR EMBL: M86722; AAC3733.1; -

DR HSSP: M80258; AAC27127.1; -

DR HSSP: P05231; 1ALU.

DR InterPro: IPR001716; -

DR Pfam: PF004489; IL6; 1.

DR PRINTS: PR00433; IL6CSFMGF.

DR PRINTS: PR00434; INTERLEUKIN_6.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.

KW Cytokine; Glycoprotein; Growth factor; Signal.

FT SIGNAL 1 29 BY SIMILARITY.

FT CHAIN 30 212 INTERLEUKIN-6.

FT DISULFID 72 78 BY SIMILARITY.

FT DISULFID 101 111 BY SIMILARITY.

FT CONFLICT 30 30 G -> E (IN REF. 2).

SEQUENCE 212 AA; 23880 MW; EF100ED030B6FDD0 CRC64;

Query Match 51.5%; Score 53; DB 1; Length 212;

Best Local Similarity 42.1%; Pred. No. 0.11;
Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFFE 19
DB 105 GFNETSCLKRLADGFFFE 123

RESULT 9

ID IL6_ORCOR STANDARD; PRT; 205 AA.
AC 028747;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
GN IL6.
OS Orctinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenkel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stolt J.L., Ferrick D.A.;
RT Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).
RT Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
CC EMBL; L46803; AAB01429.1; -
DR HSSP; P05231; IALU.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT NON_TER 1
FT SIGNAL 1
FT CHAIN 21
FT CHAIN 22 205 BY SIMILARITY.
FT DISULFID 64 70 INTERLEUKIN-6.
FT DISULFID 93 103 BY SIMILARITY.
FT CARBOHYD 164 103 BY SIMILARITY.
FT N-LINKED (GLCNAc...) (POTENTIAL).
SO SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 49.5%; Score 51; DB 1; Length 205;
Best Local Similarity 36.8%; Pred. No. 0.22;

Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFFE 19
DB 97 GFNETSCLKRLADGFFFE 115

RESULT 10
IL6_FELCA

ID IL6_FELCA STANDARD; PRT; 208 AA.
AC P41683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=94162386; PubMed=8117820;
RA Ohnishi T., Matsumoto Y., Watarai T., Gotsuka R., Tsujimoto H.,
RA Hasegawa A.;
RT Molecular cloning of feline interleukin-6 cDNA.
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RX MEDLINE=94052249; PubMed=8234373;
RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
RT Molecular cloning and characterization of a cDNA encoding feline
RT interleukin-6.
RT Proc. Soc. Exp. Biol. Med. 204:305(1993).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
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CC
CC EMBL; L16914; AAA16620.1; -
DR EMBL; D13227; BAA02507.1; -
DR HSSP; P05231; 2116.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00434; INTERLEUKIN_6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1
FT CHAIN 27
FT CHAIN 28 208
FT DISULFID 68 74
FT DISULFID 97 107
FT CONFLICT 2 2
FT CONFLICT 45 45 S -> P (IN REF. 2).
FT CONFLICT 133 133 E -> K (IN REF. 2).
FT CONFLICT 173 187 AKLOSQDEMLRITTI -> LSCSHRVAEANN (IN
FT CONFLICT 200 201 FS -> LR (IN REF. 2).
SO SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match 49.5%; Score 51; DB 1; Length 208;
Best Local Similarity 42.1%; Pred. No. 0.22;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFFE 19
DB 101 GFNETSCLKRLADGFFFE 119

RESULT 11

IL6_RAT
ID IL6_RAT STANDARD: PRT: 211 AA.
AC P20607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89380206; PubMed-2789217;
RA Northmann W, Brackak T A, Hattori M, Lee F, Fey G H;
RT "Structure of the rat interleukin 6 gene and its expression in
macrophage-derived cells."
RL J. Biol. Chem. 264:16072-16082(1989).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
PLASMACYOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M26744; AAA77659.1; -
DR EMBL; M26745; AAA41430.1; -
DR PIR; A34247; A34247.
DR HSSP; P05231; 1ALU.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GSEPMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 211
FT DISULFD 70 76
FT DISULFD 99 109
FT DISULFD 211 24357
SO SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 47.6%; Score 49; DB 1; Length 211;
Best Local Similarity 44.4%; Pred. No. 0.49;
Matches 8; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 GENETSCUKLADGFEFF 18
ID IL6_RAT 1 1 1 1 1 1
DB 103 GYNQICLKLKICGLLEF 120

RESULT 12
ID IL6_MARMO STANDARD: PRT: 207 AA.
AC O35736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.

OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Periphera blood;
RX MEDLINE-98139533; PubMed-9472070;
RA Lohrengel B, Lu M, Roggendorf M;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
and IL-6."
RL Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
PLASMACYOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
DR EMBL; Y14139; CA74571.1; -
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GSEPMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Growth factor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 207
FT DISULFD 65 71
FT DISULFD 94 104
FT DISULFD 207 23770
SO SEQUENCE 207 AA; 23770 MW; F30D19F86ADEA600 CRC64;

Query Match 46.6%; Score 48; DB 1; Length 207;
Best Local Similarity 36.8%; Pred. No. 0.7;
Matches 7; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 GENETSCUKLADGFEFF 19
ID IL6_MOUSE 1 1 1 1 1 1
DB 98 GYNRDDCLVRIRISGLERQ 116

RESULT 13
ID IL6_MOUSE STANDARD: PRT: 211 AA.
AC P08505;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL HYBRIDOMA
GROWTH FACTOR).
GN IL6 OR IL-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE-8816683; PubMed-2965020;
RA van Snick J, Cayphas S, Szikora J-P, Renaud J-C, van Roost E,
Boon T, Simpson R J;
RT "cDNA cloning of murine interleukin-HP1: homology with human
interleukin 6."
RL Eur. J. Immunol. 18:193-197(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-89035525; PubMed-3263439;
RA Tanabe O, Akira S, Kamiya T, Wong G-G, Hirano T, Kishimoto T;

"Genomic structure of the murine IL-6 gene. High degree conservation of potential regulatory sequences between mouse and human.";
 RT J. Immunol. 141:3875-3881(1988).
 RN [3]
 RC SEQUENCE FROM N.A.
 RX MEDLINE-91057159; PubMed-2243807;
 RA Grenett H.E., Fuentes N.L., Fuller G.M.;
 RT "Cloning and sequence analysis of the cDNA for murine interleukin-6.";
 RL Nucleic Acids Res. 18:6455-6455(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89017145; PubMed-3262872;
 RA Chiu C.P., Moulds C., Coffman R.L., Rennick D., Lee F.;
 RT "Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone isolated from bone marrow stromal cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).
 RN [5]
 RP SEQUENCE OF 5-211 FROM N.A.
 RC STRAIN-C57BL/60;
 RX MEDLINE-89124383; PubMed-2563387;
 RA Mock B.A., Norfan R.P., Justice M.J., Kozak C., Jenkins N.A.,
 RT Copeland N.G., Clark S.C., Wong G.G., Rudikoff S.;
 RL "The murine IL-6 gene maps to the proximal region of chromosome 5.";
 RN J. Immunol. 142:1372-1376(1989).
 RN [6]
 RP SEQUENCE OF 1-6 FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE-90171860; PubMed-2106569;
 RA Blankenstein T., Qin Z., Li W., Diamantstein T.;
 RT "DNA rearrangement and constitutive expression of the interleukin 6 gene in a mouse plasmacytoma.";
 RL J. Exp. Med. 171:965-970(1990).
 RN [7]
 RP SEQUENCE OF 25-211.
 RX MEDLINE-88329059; PubMed-3262059;
 RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
 RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence and relation to human interleukin-6.";
 RL Eur. J. Biochem. 176:187-197(1988).
 RN [8]
 RP SEQUENCE OF 66-75; 78-84 AND 128-148.
 RX MEDLINE-90147691; PubMed-2302197;
 RA Jahnke W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
 RT "Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage in polyacrylamide gels.";
 RL Biochem. Biophys. Res. Commun. 166:139-145(1990).
 RN [9]
 RP SEQUENCE OF 25-45.
 RX MEDLINE-87092311; PubMed-2948184;
 RA van Snick J., Cayphas S., Vink A., Uytendhove C., Cougle P.G.,
 RA Rubira M.R., Simpson R.J.;
 RT "Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine with growth factor activity for B-cell hybridomas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC EMBL: X06203; CAA29560.1;
 CC EMBL: M20572; AAA39302.1;
 DR

DR EMBL: X51457; CAA35824.1;
 DR EMBL: J03783; AAA39301.1;
 DR EMBL: X54542; CAA38411.1;
 DR EMBL: M24221; AAA68814.1;
 DR PIR: A30531; ICMS6.
 DR HSSP: P05231; IALU.
 DR MGD: MGI:96559; IL6.
 DR InterPro: IPR001716;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6; 1.
 DR CYTOKINE: Growth factor; Glycoprotein; Signal.
 DR FT CHAIN 25 211 INTERLEUKIN-6.
 DR FT DISULFID 70 76 BY SIMILARITY.
 DR FT DISULFID 99 109 BY SIMILARITY.
 DR SQ SEQUENCE 211 AA: BB847DDA9E86787A CRC64;
 Query Match 45.6%; Score 47; DB 1; Length 211;
 Best local similarity 38.9%; Pred. No. 1.1;
 Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 1 GFNETSCLRLKADGFEF 18
 Db 103 GYNEICLKLKISSGLLEY 120
 IL6_CAPHI STANDARD; PRT; 208 AA.
 AC Q28319;
 DT 01-NOV-1997 (rel. 35, Created)
 DT 01-NOV-1997 (rel. 35, Last sequence update)
 DT 15-JUL-1998 (rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_Taxid=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97392354; PubMed-9250586;
 RA Takakura H., Mori Y., Tatsumi M.;
 RT "Molecular cloning of caprine IL-6 cDNA and its expression in insect cells.";
 RL Int. Arch. Allergy Immunol. 113:409-416(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC EMBL: D86569; BAA13118.1;
 CC HSSP: P05231; 2116.
 CC InterPro: IPR001716;
 CC Pfam: PF00489; IL6; 1.
 CC PRINTS: PR00433; IL6GCSFNGF.
 CC PRINTS: PR00434; INTERLEUKIN6.
 CC PROSITE: PS00254; INTERLEUKIN6; 1.
 CC CYTOKINE: Glycoprotein; Growth factor; Signal.
 KM

FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 208 INTERLEUKIN-6.
 FT DISULFID 72 78 BY SIMILARITY.
 FT DISULFID 101 111 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 208 AA: 23423 MW: E92E08BF3E3230A0 CRC64;

Query Match 44.7%; Score 46; DB 1; Length 208;
 Best Local Similarity 42.1%; Pred. No. 1.5;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFEEF 19
 DB 105 GFNOAICLKRTTAGLEXYO 123

RESULT 15
 IL6_SHEEP STANDARD: PRT; 208 AA.
 AC P29455;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 ON NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94041419; PubMed=8225400;
 RA Andrews A.E., Barclay G.J., Ashman K., Meusen E.N.T., Brandon M.R.,
 RA Nash A.D.;
 RT "Molecular cloning and characterization of a ruminant Interleukin-6
 RT cDNA."
 RL Immunol. Cell Biol. 71:341-348(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ebrahimi B.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC
 CC -----
 DR EMBL: X62501: CAA44363.1; -;
 DR EMBL: X68723: CAA48662.1; -;
 DR EMBL: A19159: CAA01443.1; -;
 DR PIR: S29549; S29549.
 DR HSSP: P05231; 2116.
 DR InterPro: IPR001716; -;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN_6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 208 INTERLEUKIN-6.
 FT DISULFID 72 78 BY SIMILARITY.
 FT DISULFID 101 111 BY SIMILARITY.

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 4 4 L -> R (IN REF. 2).
 FT CONFLICT 110 110 I -> V (IN REF. 2).
 FT CONFLICT 171 171 M -> L (IN REF. 2).
 FT CONFLICT 201 201 S -> R (IN REF. 2).
 SQ SEQUENCE 208 AA: 23446 MW: EEC996C13E3230A0 CRC64;

Query Match 44.7%; Score 46; DB 1; Length 208;
 Best Local Similarity 42.1%; Pred. No. 1.5;
 Matches 8; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 GFNETSCLKRLADGFFEEF 19
 DB 105 GFNOAICLKRTTAGLEXYO 123

Search completed: October 4, 2001, 19:12:32
 Job time: 267 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:11:56 ; Search time 74.43 Seconds
(without alignments)
33.774 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105
Perfect score: 103
Sequence: 1 GENETSCIKLADGFFEE 19

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_TREMBL_16:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	204	14	040918 Kaposi's sa
2	103	100.0	204	14	098823 Kaposi's sa
3	62	60.2	160	6	097535 actus vocif
4	62	60.2	175	6	097TH4 actus nigri
5	61	59.2	209	6	097540 actus nancy
6	61	59.2	209	6	097TH3 actus lemur
7	53	51.5	207	6	09MYZ7 canis famli
8	51	49.5	208	6	09XT80 delphinapte
9	49	47.6	207	11	09JHH3 marmota mon
10	48	46.6	162	2	09KDM5 bacillus ha
11	47	45.6	745	10	081733 arabisopsis
12	46	44.7	568	2	09KK17 vibrio cnoi
13	45.5	44.2	492	2	09S0L2 shewanella
14	45	43.7	148	7	09XRE6 ovis aries
15	45	43.7	207	6	028403 embryda lut
16	45	43.7	484	1	058908 pyrococcus
17	44	42.7	191	2	09S4A6 actinobacil
18	44	42.7	204	10	09FK11 arabidopsis
19	44	42.7	282	2	051358 borrella bu

20	44	42.7	454	5	09XWLO	09xw10 caenorhabdi
21	44	42.7	1609	5	09GRC3	09grc3 caenorhabdi
22	44	42.7	1893	5	017887	017887 caenorhabdi
23	43	41.7	157	1	026871	026871 methanobact
24	43	41.7	231	2	09KGE5	09kge5 bacillus ha
25	43	41.7	763	2	09E2B6	09ezb6 zymomonas m
26	43	41.7	1714	10	09FWM3	09fwm3 arabidopsis
27	42.5	41.3	492	5	027470	027470 caenorhabdi
28	42	40.8	180	2	09W80	09w80 thermotoga
29	42	40.8	219	5	016639	016639 caenorhabdi
30	42	40.8	309	11	008763	008763 rattus norv
31	42	40.8	364	5	021590	021590 caenorhabdi
32	42	40.8	460	4	095523	095523 homo sapien
33	42	40.8	481	4	09Y3J7	09y3j7 homo sapien
34	42	40.8	609	4	09NZM7	09nzm7 homo sapien
35	42	40.8	753	4	025175	025175 homo sapien
36	42	40.8	948	5	09V9C5	09v9c5 drosophila
37	42	40.8	1573	11	09QXL2	09qxl2 mus muscula
38	42	40.8	1690	5	044929	044929 drosophila
39	42	40.8	1690	5	09VJES	09vj65 drosophila
40	42	40.8	1980	14	084185	084185 human paral
41	42	40.8	2223	14	09WFE25	09wfe25 human paral
42	42	40.8	2228	14	098705	098705 sendai viru
43	42	40.8	2258	14	081081	081081 human paral
44	42	40.8	2258	14	089238	089238 human paral
45	41.5	40.3	350	10	09FF04	09ffc4 cicor arlet

ALIGNMENTS

RESULT 1
ID 040918 PRELIMINARY; PRT; 204 AA.

AC 040918; 040918; (TREMREL. 05, Created)
DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)
DE ORF K2.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
CC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_taxid=37296;
RN [1]
RP MEDLINE-97138401; PubMed-8985427;
RA Neipel F., Albrecht J.C., Fleckenstein B.;
RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
human herpesvirus 8: determinants of its pathogenicity?";
RL J. Virol. 71:4187-4192(1997).
DR EMBL; U93872; AAB62676.1; -;
DR InterPro; IPR003573; -;
DR InterPro; IPR003574; -;
DR Pfam; PF00489; IL6; 1.
DR PRODOM; PD004356; -; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 204 AA; 23408 MW; 2F46737828AF20B9 CRC64;

Query Match 100.0%; Score 103; DB 14; Length 204;

Best Local Similarity 100.0%; Pred. No. 2.5e-09;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GENETSCIKLADGFFEE 19
DB 87 GENETSCIKLADGFFEE 105

```

RESULT 2
ID 098823 PRELIMINARY: PRT: 204 AA.
AC 098823:
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 HOMOLOG (FRAGMENT).
GN IL-6.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RA Nelpel F., Albrecht J.C., Essner A., Huang Y.Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nicholas J., Ruvolo V.R., Burns M.H., Sandford G., Wan X., Clufo D.,
RA Hendrickson S., Guo H.G., Hayward G.S., Reitz M.S.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE-97094384; PubMed-8939871;
RA Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV.";
RL Science 274:1739-1744(1996).
RN [4]
RP SEQUENCE FROM N.A.
RA MEDLINE-97121480; PubMed-8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Petruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [5]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Petruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Sun R., Lin S.-F., Miller G.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U73655; AAB18244.1; -
DR EMBL: U67774; AAB61701.1; -
DR EMBL: U75698; AAC57089.1; -
DR EMBL: U71365; AAC34937.1; -
DR InterPro: IPR003573; -
DR Pfam: PF00489; IL6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 204
SQ SEQUENCE 204 AA: 23408 MW: 1CA7772A0EDC05EB CRC64;

```

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Query Match 100.0%; Score 103; DB 14; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.5e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GFNETSCLKLADGPFPE 19
DB 87 GFNETSCLKLADGPFPE 105

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RESULT 3
ID 097535 PRELIMINARY: PRT: 160 AA.
AC 097535:
DT 01-MAY-1999 (TEMBLrel. 10, Created)
DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patatroyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different Interleukin genes
RT in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014505; AAD01531.1; -
DR HSSP: P05231; IL6.
DR InterPro: IPR003573; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFEMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 160 AA: 17855 MW: 07A021338650A46D CRC64;

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```

Query Match 60.2%; Score 62; DB 6; Length 160;
Best Local Similarity 57.9%; Pred. No. 0.012;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
OY 1 GFNETSCLKLADGPFPE 19
DB 105 GFNETSCLKLADGPFPE 123

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RESULT 4
ID 097TH4 PRELIMINARY: PRT: 175 AA.
AC 097TH4:
DT 01-MAY-2000 (TEMBLrel. 13, Created)
DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patatroyo M.E.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF093322; AAF21297.1; -
DR HSSP: P05231; IL6.
DR InterPro: IPR002069; -
DR InterPro: IPR003573; -
DR InterPro: IPR003574; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFEMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00243; -; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1

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SO SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match

Best Local Similarity 60.2%; Score 62; DB 6; Length 175;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFEFE 19

Db 105 GFNETSCLKRLADGFFEFE 123

RESULT 5

ID 097540 PRELIMINARY; PRT; 209 AA.

AC 097540; 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DE 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE INTERLEUKIN-6 (FRAGMENT).

IL-6.

GN Aotus nancymae (Owl monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=37293;

RN [1]

RP SEQUENCE FROM N.A.

RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;

RT "Identification, cloning and sequencing of different interleukin genes

in 4 Aotus species."

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF014510; AAD01536.1;

DR HSSP; P05231; IALU.

DR InterPro; IPR003573;

DR InterPro; IPR003574;

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

FT NON_TER 1 1

FT NON_TER 209 209

SO SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match

Best Local Similarity 59.2%; Score 61; DB 6; Length 209;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFEFE 19

Db 105 GFNETSCLKRLADGFFEFE 123

RESULT 6

ID 097TH3 PRELIMINARY; PRT; 209 AA.

AC 097TH3; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE INTERLEUKIN-6 (FRAGMENT).

IL-6.

GN Aotus lemurinus (Northern gray-necked night monkey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.

OX NCBI_TaxID=31147;

RN [1]

RP SEQUENCE FROM N.A.

RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.;

RT "Aotus lemurinus gene for IL-6."

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF097323; AAF21298.1; -.

DR HSSP; P05231; IALU.

DR InterPro; IPR003573; -.

DR InterPro; IPR003574; -.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

FT NON_TER 1 1

FT NON_TER 209 209

SO SEQUENCE 209 AA; 23115 MW; A0A3DFAA4BF560CC CRC64;

Query Match

Best Local Similarity 59.2%; Score 61; DB 6; Length 209;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFEFE 19

Db 105 GFNETSCLKRLADGFFEFE 123

RESULT 7

ID 09MYZ7 PRELIMINARY; PRT; 207 AA.

AC 09MYZ7; 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE INTERLEUKIN-6.

IL-6.

GN Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RA Youn H.-Y., Shin I.-S.;

RT "Canine IL-6 mRNA."

RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF275796; AAE86275.1; -.

DR InterPro; IPR003573; -.

DR InterPro; IPR003574; -.

DR Pfam; PF00489; IL6; 1.

DR PRINTS; PR00433; IL6GCSFMGF.

DR PRINTS; PR00434; INTERLEUKIN.

DR PROSITE; PS00254; INTERLEUKIN_6; 1.

DR SMART; SM00126; IL6; 1.

SO SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

Query Match

Best Local Similarity 51.5%; Score 53; DB 6; Length 207;

Matches 8; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFEFE 19

Db 100 GFNETSCLKRLADGFFEFE 118

RESULT 8

ID 09XT80 PRELIMINARY; PRT; 208 AA.

AC 09XT80; 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE INTERLEUKIN 6 PRECURSOR.

OS Delphinapterus leucas (Beluga whale).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;

OC Monodontidae; Delphinapterus.

OX NCHL_TaxID-9749;
 RN 111
 RP SEQUENCE FROM N.A.
 RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
 RT "Molecular cloning and phylogenetic analysis of beluga whale
 (Delphinapterus leucas) Interleukin 6."
 RL Submitted (Jul-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF076643; AAD42929.1; -.
 DR HSSP: P05231; IALU.
 DR InterPro: IPR003573; -.
 DR InterPro: IPR003574; -.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match 49.5%; Score 51; DB 6; Length 208;
 Best Local Similarity 36.8%; Pred. No. 1;
 Matches 7; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

OY 1 GENETSCCLKLADGFFEEF 19
 111:111:111:111:
 DB 100 GFMQETCLMRITTCGLLEFQ 118

RESULT 9
 O9JHH3 PRELIMINARY; PRT: 207 AA.
 ID O9JHH3
 AC O9JHH3
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OX NCBI_TaxID-9995;
 RN 111
 RP SEQUENCE FROM N.A.
 RA TISSUE-PERIPHERAL BLOOD;
 RL LI D.H., Cullen J.M.;
 RT "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis."
 RL Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA LI D.H., Cullen J.M.;
 RT Gene Structure of the Woodchuck Interleukin-6."
 RL Submitted (Jan-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF012908; AAF34861.1; -.
 DR EMBL: AF122896; AAF28873.1; -.
 DR InterPro: IPR003573; -.
 DR InterPro: IPR003574; -.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA; 23645 MW; ADZFA6E450E13470 CRC64;

Query Match 47.6%; Score 49; DB 11; Length 207;
 Best Local Similarity 36.8%; Pred. No. 2.2;
 Matches 7; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 1 GENETSCCLKLADGFFEEF 19
 111:111:111:111:
 DB 98 GYRNCILVITTSGLLEFQ 116

RESULT 10
 O9KDM5 PRELIMINARY; PRT: 162 AA.
 ID O9KDM5
 AC O9KDM5
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE BH1096 PROTEIN.
 GN BH1096.
 OS Bacillus halodurans.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID-86653;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-C-125 / JCM 9153;
 RA Takami H., Nakasone K., Takaki Y.;
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF001510; BAB04815.1; -.
 SQ SEQUENCE 162 AA; 19156 MW; F03A098FEA1FAB73 CRC64;

Query Match 46.6%; Score 48; DB 2; Length 162;
 Best Local Similarity 66.7%; Pred. No. 2.5;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 TSCCLKLADGFFEEF 19
 111:111:111:111:
 DB 31 TSMIEIGADGFFEEF 45

RESULT 11
 O81733 PRELIMINARY; PRT: 745 AA.
 ID O81733
 AC O81733
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE HYPOTHETICAL 83.1 KDa PROTEIN.
 GN F16620.70 OR AT4G23370.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
 OC Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID-3702;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Watson M.D., Gibbons T., Bartley J., Bancroft I., Mewes H.W.,
 RA Mayer K.F.X., Scheller C., Bevan M.;
 RL Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.
 RN 121
 RP SEQUENCE FROM N.A.
 RA Watson M.D., Gibbons T., Bartley J., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 RN 131
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AL013326; CAZ0458.1; -.
 DR EMBL: AL161559; CAB79292.1; -.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 745 AA; 83092 MW; 45BFA5A79B210299 CRC64;

Query Match 45.6%; Score 47; DB 10; Length 745;
 Best Local Similarity 47.1%; Pred. No. 18;
 Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

OY 1 GENETSCCLKLADGFFEEF 17
 111:111:111:111:
 DB 289 GPNKTCYNTLCPGFVQ 305

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RESULT 12
09KRL7 PRELIMINARY: PRT: 568 AA.
AC 09KRL7;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE RESPONSE REGULATOR.
GN VCA1086.
OS Vibrio Cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EL TOR N16961 / SEROTYPE O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Drysdale J., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nieman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
DR EMBL: AE004434; AAF96979.1; -.
DR TIGR: VCA1086; -.
DR InterPro: IPR001789; -.
DR InterPro: IPR003588; -.
DR Pfam: PF00072; response_reg. 1.
DR SMART: SM00331; PP2C_SIG. 1.
SQ SEQUENCE 568 AA; 64331 MW; 87A02A350D986F51 CRC64;

Query Match 44.7%; Score 46; DB 2; Length 568;
Best Local Similarity 69.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 SCLKKLADGFFEF 18
ID 09S0L2 PRELIMINARY: PRT: 492 AA.
AC 09S0L2;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE RNA POLYMERASE SIGMA-54 FACTOR.
GN RPN.
OS Shewanella Violacea.
OC Bacteria; Proteobacteria; gamma subdivision; Alteromonadaceae;
OC Shewanella.
OX NCBI_TaxID=60217;
RN [1]
RP SEQUENCE FROM N.A.
RC Ikegami A., Nakasone K., Fujita M., Fujii S., Kato C., Usami R.,
RA Horikoshi K.;
RT Isolation and molecular characterization of the gene encoding RNA
RT polymerase sigma factor sigma54 of deep-sea piezophilic Shewanella
RT violacea.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE SIGMA FACTOR IS AN INITIATION FACTOR THAT PROMOTES
CC ATTACHMENT OF THE RNA POLYMERASE TO SPECIFIC INITIATION SITES AND
CC THEN IS RELEASED (BY SIMILARITY).
CC -!- SIMILARITY: TO THE SIGMA-54 FACTOR FAMILY.
DR EMBL: AB033988; BAA85885.1; -.
DR InterPro: IPR000394; -.

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DR Pfam: PF00309; Sigma54_factors. 1.
DR PRINTS: PR00045; SIGMA54FCV.
DR PROSITE: PS00717; SIGMA54_1; 1.
DR PROSITE: PS00718; SIGMA54_2; 1.
DR PROSITE: PS50044; SIGMA54_3; 1.
KW DNA-binding; DNA-directed RNA polymerase; Sigma factor;
KW transcription regulation.
SQ SEQUENCE 492 AA; 55359 MW; 8B95B22C706DF7F7 CRC64;

Query Match 44.2%; Score 45.5; DB 2; Length 492;
Best Local Similarity 47.6%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 5; Indels 5; Gaps 1;

QY 3 NET-----SCLKKLADGFFEF 18
ID 09XRE6 PRELIMINARY: PRT: 148 AA.
AC 09XRE6;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN OLA-DQ2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MERINO;
RX MEDLINE=97083726; PubMed=8930070;
RA Escaya A.P., Hickford J.C., Montgomery G.W., Dodds K.G., Bullock D.W.;
RT Polymorphism at the ovine major histocompatibility complex class II
RT loci.";
RL Anim. Genet. 27:305-312(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MERINO;
RA Slow S., Ridgway H.J., Hickford J.G.H.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF129118; AAD3404.1; -.
DR HSP; P01888; IBMG.
DR InterPro: IPR001003; -.
DR InterPro: IPR003006; -.
DR InterPro: IPR003597; -.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00993; MHC_II_alpha; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SMART: SM00407; IgC1; 1.
FT NON_TER 1
FT NON_TER 148
FT SEQUENCE 148 AA; 16852 MW; F31FE0608CD7ED07 CRC64;

Query Match 43.7%; Score 45; DB 7; Length 148;
Best Local Similarity 55.6%; Pred. No. 7.2;
Matches 10; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKLADGFFEF 18
ID 111 GVSETSLPDDDDFFEF 128
DB 111 GVSETSLPDDDDFFEF 128

RESULT 15
Q28403

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ID 028403 PRELIMINARY: PRT: 207 AA.
AC 028403:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Enhydra lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pissipedia; Mustelidae; Enhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stolt J.L., Ferrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
DR EMBL; L46804; AAB01428.1; -.
DR HSSP; P05231; IL6.
DR InterPro: IPR003573; -.
DR InterPro: IPR003574; -.
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GSPMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 207 AA: 23527 MW: 729E0CD91136D8B CRC64;

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Query Match 43.7%; Score 45; DB 6; Length 207;
Best Local Similarity 38.9%; Pred. No. 10;
Matches 7; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
OY 2 ENETSCLKKLADGFFEE 19
DB 103 PNOETCLTRITTCLOEFQ 120

```

Search completed: October 4, 2001, 19:11:58
 Job time: 1184 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; Search time 32.27 Seconds
(without alignments)
12.123 Million cell updates/sec

Title: US-09-230-048-2_COPY_87_105
Perfect score: 103
Sequence: 1 GENETSCIKLADGFFEE 19

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/5B.COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6A.COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	103	100.0	185	3 US-09-122-443-16	Sequence 16, Appl
2	61	59.2	162	2 US-08-716-317-10	Sequence 10, Appl
3	61	59.2	163	2 US-08-716-317-15	Sequence 15, Appl
4	61	59.2	164	1 US-08-318-193-60	Sequence 60, Appl
5	61	59.2	167	1 US-08-246-427A-2	Sequence 2, Appl
6	61	59.2	167	2 US-08-766-620-2	Sequence 2, Appl
7	61	59.2	167	5 PCT-US95-06094-2	Sequence 21, Appl
8	61	59.2	172	4 US-08-149-101A-21	Sequence 21, Appl
9	61	59.2	172	5 PCT-US94-12873-21	Sequence 20, Appl
10	61	59.2	174	4 US-08-149-101A-20	Sequence 20, Appl
11	61	59.2	174	5 PCT-US94-12873-20	Sequence 20, Appl
12	61	59.2	183	1 US-08-009-973-1	Sequence 1, Appl
13	61	59.2	184	1 US-08-567-047-2	Sequence 2, Appl
14	61	59.2	184	2 US-08-693-182-2	Sequence 2, Appl
15	61	59.2	184	2 US-08-567-048-2	Sequence 2, Appl
16	61	59.2	184	2 US-09-008-482-2	Sequence 2, Appl
17	61	59.2	184	2 US-08-945-529-8	Sequence 8, Appl
18	61	59.2	184	2 US-08-945-529-9	Sequence 9, Appl
19	61	59.2	184	2 US-08-945-529-10	Sequence 10, Appl
20	61	59.2	184	2 US-08-945-529-11	Sequence 11, Appl
21	61	59.2	184	2 US-08-945-529-12	Sequence 12, Appl
22	61	59.2	184	4 US-08-149-101A-17	Sequence 17, Appl
23	61	59.2	184	4 US-08-149-101A-22	Sequence 22, Appl
24	61	59.2	184	5 PCT-US94-12873-17	Sequence 17, Appl
25	61	59.2	184	5 PCT-US94-12873-22	Sequence 22, Appl
26	61	59.2	184	6 PCT-US94-12873-22	Sequence 22, Appl
27	61	59.2	185	1 US-07-632-070B-1	Sequence 1, Appl

28	61	59.2	185	1 US-07-918-181A-2	Sequence 2, Appl
29	61	59.2	185	1 US-07-918-181A-4	Sequence 4, Appl
30	61	59.2	185	1 US-07-918-181A-6	Sequence 6, Appl
31	61	59.2	185	1 US-07-918-181A-8	Sequence 8, Appl
32	61	59.2	185	1 US-08-231-575-2	Sequence 2, Appl
33	61	59.2	185	1 US-08-231-575-4	Sequence 4, Appl
34	61	59.2	185	1 US-08-231-575-6	Sequence 6, Appl
35	61	59.2	185	1 US-08-231-575-8	Sequence 8, Appl
36	61	59.2	185	1 US-08-246-427A-5	Sequence 5, Appl
37	61	59.2	185	2 US-08-716-317-7	Sequence 7, Appl
38	61	59.2	185	2 US-08-766-620-5	Sequence 5, Appl
39	61	59.2	185	5 PCT-US92-05612-2	Sequence 2, Appl
40	61	59.2	185	5 PCT-US93-06928-2	Sequence 2, Appl
41	61	59.2	185	5 PCT-US93-06928-4	Sequence 4, Appl
42	61	59.2	185	5 PCT-US93-06928-6	Sequence 6, Appl
43	61	59.2	185	5 PCT-US93-06928-8	Sequence 8, Appl
44	61	59.2	185	6 PCT-US93-06928-8	Sequence 8, Appl
45	61	59.2	186	1 US-07-632-070B-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-122-443-16
: Sequence 16, Application US/09122443
: Patent No. 6060284
GENERAL INFORMATION:
: APPLICANT: Bazar, J. Fernando
: TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
: NUMBER OF SEQUENCES: 16
: CORRESPONDENCE ADDRESS:
: ADDRESS: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/122,443
: FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/053,765
: FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
: TELEPHONE: (650)852-9196
: TELEFAX: (650)466-1200
INFORMATION FOR SEQ ID NO: 16:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 185 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-09-122-443-16

Query Match 100.0%; Score 103; DB 3; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.2e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GENETSCIKLADGFFEE 19
|||||

Db 68 GFNETSCLKADGPFEE 86

RESULT 2

US-08-716-317-10

Sequence 10, Application US/08716317

Patent No. 5919654

GENERAL INFORMATION:

APPLICANT: HAMA, YUKO

APPLICANT: TOHDA, HIDEKI

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: NIKAI, KIYOKAZU

APPLICANT: KUMAGAI, HIROMICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

TITLE OF INVENTION: VECTOR CONTAINING IT

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/716,317

FILING DATE: 02-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OHLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-716-317-10

Query Match 59.2%; Score 61; DB 2; Length 162;

Best local Similarity 57.9%; Pred. No. 0.0074;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKADGPFEE 19

Db 55 GFNETSCLKADGPFEE 73

RESULT 3

US-08-716-317-15

Sequence 15, Application US/08716317

Patent No. 5919654

GENERAL INFORMATION:

APPLICANT: HAMA, YUKO

APPLICANT: TOHDA, HIDEKI

APPLICANT: TSUKAMOTO, HIROKO

APPLICANT: NIKAI, KIYOKAZU

APPLICANT: KUMAGAI, HIROMICHI

TITLE OF INVENTION: SECRETION SIGNAL GENE AND EXPRESSION

TITLE OF INVENTION: VECTOR CONTAINING IT

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: OHLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESS: P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/716,317

FILING DATE: 02-OCT-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/00198

FILING DATE: 01-FEB-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 17167/1995

FILING DATE: 03-FEB-1996

ATTORNEY/AGENT INFORMATION:

NAME: OHLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 59-924-0 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 163 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-716-317-15

Query Match 59.2%; Score 61; DB 2; Length 163;

Best local Similarity 57.9%; Pred. No. 0.0075;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKADGPFEE 19

Db 56 GFNETSCLKADGPFEE 74

RESULT 4

US-08-318-193-60

Sequence 60, Application US/08318193

Patent No. 5641663

GENERAL INFORMATION:

APPLICANT: GARVIN, Robert T.

APPLICANT: MAIER, Lawrence T.

TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION

TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY

TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 1800 Diagonal Road, Suite 500

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,193
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,314
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 18740/116 CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 164 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-318-193-60

Query Match 59.2%; Score 61; DB 1; Length 164;
Best Local Similarity 57.9%; Pred. No. 0.0075;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENETSCCLKADGFFERE 19
||||:||||:|
DB 57 GFNETCLVKIITGLERE 75

RESULT 5
US-08-246-427A-2
Sequence 2, Application US/08246427A
Patent No. 5641657
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,427A
FILING DATE: Submitted herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-
TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-246-427A-2

Query Match 59.2%; Score 61; DB 1; Length 167;
Best Local Similarity 57.9%; Pred. No. 0.0077;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENETSCCLKADGFFERE 19
||||:||||:|
DB 60 GFNETCLVKIITGLERE 78

RESULT 6
US-08-766-620-2
Sequence 2, Application US/08766620
Patent No. 5958400
GENERAL INFORMATION:
APPLICANT: RUBEN, ET AL.
TITLE OF INVENTION: Interleukin-6 Splice Variant
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,620
FILING DATE: December 12, 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/246,427
FILING DATE: MAY 19, 1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-593 (PF120)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-766-620-2

Query Match 59.2%; Score 61; DB 2; Length 167;
Best Local Similarity 57.9%; Pred. No. 0.0077;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GENETSCCLKADGFFERE 19
||||:||||:|

Db 60 GFNETCLVKIITGLLEFE 78

RESULT 7

PCT-US95-06094-2

Sequence 2, Application PC/TUS9506094

GENERAL INFORMATION:

APPLICANT: RUBEN, ET AL.

TITLE OF INVENTION: Interleukin-6 splice variant

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

STREET: 6 BECKER FARM ROAD

CITY: ROSELAND

STATE: NEW JERSEY

COUNTRY: USA

ZIP: 07068

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 INCH DISKETTE

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WORD PERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06094

FILING DATE: Submitted herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/246,427

FILING DATE: MAY 19, 1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: FERRARO, GREGORY D.

REGISTRATION NUMBER: 36,134

REFERENCE/DOCKET NUMBER: 325800-

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-994-1700

TELEFAX: 201-994-1744

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 167 AMINO ACIDS

TYPE: AMINO ACID

STRANDEDNESS:

TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN

PCT-US95-06094-2

Query Match 59.2%; Score 61; DB 5; Length 167;

Best Local Similarity 57.9%; Pred. No. 0.0077; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

RESULT 8

US-08-149-101A-21

Sequence 21, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,101A

FILING DATE: 8-No. 6171824-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/097,869

FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oster, Jeffrey B. and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)282-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 172

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORGANISM: homo sapien

US-08-149-101A-21

Query Match 59.2%; Score 61; DB 4; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 78 GFNETCLVKIITGLLEFE 96

RESULT 9

PCT-US94-12873-21

Sequence 21, Application PC/TUS9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12873

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 172

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-12873-21

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

Query Match 59.2%; Score 61; DB 5; Length 172;

Best Local Similarity 57.9%; Pred. No. 0.0079; 6; Indels 0; Gaps 0;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 GFNETSCLKRLADGFFFE 19

Db 60 GFNETCLVKIITGLLEFE 78

Db 78 GFNETCLVKITIGLEFE 96

RESULT 10

US-08-149-101A-20

Sequence 20, Application US/08149101A

Patent No. 6171824

GENERAL INFORMATION:

APPLICANT: Todaro, George J.

APPLICANT: Leung, David W.

APPLICANT: Rose, Timothy M.

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cell Therapeutics, Inc.

STREET: 200 Elliott Avenue West, Suite 400

CITY: Seattle

STATE: Washington

COUNTRY: U.S.A.

ZIP: 98119

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" disk, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/149,101A

FILING DATE: 8-No. 6171824-1993

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US08/097,869

FILING DATE: 27-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oster, Jeffrey B. and Faciszewski, Stephen

REGISTRATION NUMBER: 32,585 and 36,131, respectively

REFERENCE/DOCKET NUMBER: 0105A

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206)284-7100

TELEFAX: (206)284-6206

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 174

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHEICAL: no

ANTI-SENSE: no

FRAGMENT TYPE:

ORIGINAL SOURCE:

ORGANISM: homo sapien

US-08-149-101A-20

Query Match 59.2%; Score 61; DB 4; Length 174;

Best Local Similarity 57.9%; Pred. No. 0.008;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETCLVKADGFEFE 19

Db 78 GFNETCLVKITIGLEFE 96

RESULT 11

PCT-US94-12873-20

Sequence 20, Application PC/TUS9412873

GENERAL INFORMATION:

APPLICANT:

APPLICANT:

APPLICANT:

TITLE OF INVENTION: HYBRID CYTOKINES

NUMBER OF SEQUENCES: 26

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" diskette, 1.44mb, double side, high density

COMPUTER: AST-IBM Compatible

OPERATING SYSTEM: MS-DOS Version 6

SOFTWARE: WORD for WINDOWS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/12873

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 174

TYPE: amino acid

TOPOLOGY: linear

PCT-US94-12873-20

Query Match 59.2%; Score 61; DB 5; Length 174;

Best Local Similarity 57.9%; Pred. No. 0.008;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETCLVKADGFEFE 19

Db 78 GFNETCLVKITIGLEFE 96

RESULT 12

US-08-009-973-1

Sequence 1, Application US/08009973

Patent No. 533834

GENERAL INFORMATION:

APPLICANT: WILLIAMS, Ashley M.

TITLE OF INVENTION: Ultrapure Human Interleukin-6

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/009,973

FILING DATE: 19930126

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 16777/199 ALLE

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 183 amino acids

TYPE: AMINO ACID

TOPOLOGY: linear

US-08-009-973-1

Query Match 59.2%; Score 61; DB 1; Length 183;

Best Local Similarity 57.9%; Pred. No. 0.0085;

Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETCLVKADGFEFE 19

Db 76 GFNETCLVKITIGLEFE 94

RESULT 13

US-08-567-047-2
Sequence 2, Application US/08567047
Patent No. 5789552
Patent No. 5789552 5789555
GENERAL INFORMATION:
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Gennaro
TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,047
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-047-2

Query Match 59.2%; Score 61; DB 1; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKADGPFEE 19
DB 77 GFNETCLVKIITGLLEFE 95

RESULT 14
US-08-693-182-2
Sequence 2, Application US/08693182
Patent No. 5849283
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: TONITTI, Carlo
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPRANTAGONISTS OF HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: Browdy and Netmark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A000805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CILIBERTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-693-182-2

Query Match 59.2%; Score 61; DB 2; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLKKADGPFEE 19
DB 77 GFNETCLVKIITGLLEFE 95

RESULT 15
US-08-567-048-2
Sequence 2, Application US/08567048
Patent No. 5891998
GENERAL INFORMATION:
APPLICANT: SAVINO, Rocco
APPLICANT: LAHM, Armin
APPLICANT: CILIBERTO, Gennaro
TITLE OF INVENTION: METHOD FOR SELECTING SUPERAGONISTS,
TITLE OF INVENTION: ANTAGONISTS AND SUPRANTAGONISTS FOR HORMONES HAVING
TITLE OF INVENTION: GP 130 AS PART OF THEIR RECEPTOR COMPLEX
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,048

FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 184 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-567-048-2

Query Match 59.2%; Score 61; DB 2; Length 184;
Best Local Similarity 57.9%; Pred. No. 0.0085;
Matches 11; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 GFNETSCLTKRIADGFEFE 19
Db 77 GFNETCLVKITGLLEFE 95

Search completed: October 4, 2001, 19:10:32
Job time: 1163 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:08 ; Search time 54.44 Seconds
(without alignments)
236.082 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071
Sequence: 1 MNSFSTSAFGPYAFSLGLL.....LILRSFKFELQSLRALROM 212

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1071	100.0	212	8 AAP70238	Interferon-beta 2a
2	1071	100.0	212	9 AAP80269	Recombinant interl
3	1071	100.0	212	10 AAP90047	PBSF2-L8 sequence.
4	1071	100.0	212	10 AAP90371	PBSF2-L8. AAP903
5	1071	100.0	212	10 AAP90436	Interferon-beta-2.
6	1071	100.0	212	10 AAP90469	Interleukin-6. Ho
7	1071	100.0	212	11 AAR05415	Human B-cell diffe
8	1071	100.0	212	14 AAR33430	IFN-beta-2a. Homo
9	1071	100.0	212	14 AAR34726	Human IL-6 (for mo
10	1071	100.0	212	15 AAR49041	Human Interleukin
11	1071	100.0	212	15 AAR49249	Sequence of human

12	1071	100.0	212	16 AAR72317	Interferon-beta2A.
13	1071	100.0	212	21 AAY87816	Human IL-6 protein
14	1068	99.7	212	9 AAP81156	Human B-cell diffe
15	1065	99.4	212	9 AAP82577	Leader sequence of
16	1065	99.4	212	9 AAP81176	Sequence of the BS
17	1065	99.4	212	10 AAP90121	Human lymphocyte r
18	1063	99.3	212	14 AAR33384	Cytokine hIL-6. H
19	1063	99.3	212	22 AAB49786	Human interferon B
20	1046	97.7	212	12 AAR12521	B cell differentia
21	1045	97.6	212	18 AAW35878	Human Interleukin-
22	1045	97.6	212	18 AAR33643	Human Interleukin-
23	1036	96.7	211	13 AAR25279	Human Interleukin-
24	1002.5	93.6	201	9 AAP81162	Mutant human BCDP.
25	955	89.2	188	20 AAW95011	Polypeptide with B
26	948	88.5	196	18 AAW36848	Human Interleukin-
27	943.5	88.1	208	9 AAP81160	Human fusion polyp
28	942	88.0	515	21 AAB15404	Polypeptide with B
29	938.5	87.6	543	20 AAY03164	IL-6R/IL-6 fusion
30	938	87.6	185	9 AAP81159	Chimeric sIL-6R/IL
31	938	87.6	185	11 AAR05275	Polypeptide with B
32	938	87.6	185	15 AAR45717	Segment of human B
33	938	87.6	185	16 AAR68624	Full length interl
34	938	87.6	186	9 AAP80270	Ala-BCDF. Homo sa
35	938	87.6	186	16 AAR79339	Recombinant interl
36	938	87.6	186	16 AAR75765	PMON13040 peptide.
37	938	87.6	186	21 AAY53220	Human Interleukin-
38	938	87.6	187	12 AAR13471	Human G-CSF mutant
39	938	87.6	317	16 AAR79321	hIL-6 protein. Ho
40	938	87.6	317	16 AAR79322	IL-3 containing fu
41	938	87.6	347	22 AAB73222	Human Interleukin-
42	937.5	87.5	208	10 AAP94755	Fusion protein Npr
43	936	87.4	185	15 AAR45719	Sequence of varian
44	934	87.2	184	9 AAP81158	Full length interl
45	934	87.2	184	15 AAR52556	Polypeptide with B

ALIGNMENTS

RESULT 1
ID AAP70238 standard; protein: 212 AA.
XX
AC AAP70238;
XX
DC 21-MAR-1980 (first entry)
XX
DE Interferon-beta 2a.
XX
KW Interferon-beta 2a; therapy;
XX
OS Homo sapiens.
XX
PN EP220574-A.
XX
PD 06-MAY-1987.
XX
PE 10-OCT-1986; 86EP-0114049.
XX
PR 08-MAY-1986; 86US-0860883.
PR 14-OCT-1985; 85IL-0076714.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Revel M, Zilberstei A;
XX
DR WPI; 1987-124210/18.
XX
N-PSDB; AAN70348.
XX
PT Recombinant human Interferon-beta(2a) and beta(2b) - useful for
PT inflammation, acute phase response or regulation of cell
XX proliferation
XX

PS Disclosure; fig. 1; 17pp; English.
 XX
 CC The protein has interferon activity. It inhibits viral replication and
 CC cytopathic effect and induces the proteins typical of the biological
 CC response of human cells to interferon. It is useful for influencing
 CC cell growth and differentiation, esp. during terminal differentiation of
 CC tumour cells and for inhibiting fibroblast proliferation and to prevent
 CC sclerosis after infection. The protein is also useful in the fields of
 CC inflammation acute-phase response or regulation of cell proliferation.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 8; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTASGPVAFSLGLLVLPAPAPVPPGDSKDVAAPRROPVLTSSERIDKQIRYI 60
 DB 1 mnsfstasgvpafslgllvlpapapvpvppgdskdvaaprrpvtsseridkqiryi 60
 QY 61 LDGISALRKETCKSNMCESSKEALAEENNLPRMAEKDGCFOGSGFNEETCLVKITIGLL 120
 DB 61 ldgisalrketcksnmcesskealaennlprmaekdgcfgsgfneetclvkiitgll 120
 QY 121 EEFVYLEYIQNRRSESEDOARAVOMSTKVIQFLOKKAKNLDAITPPDPTTNASLITKIQ 180
 DB 121 eefvyleyiqnrrseeseoavomstkvilqflokaknldaitppdpttnaslitkiq 180
 QY 181 AONQWLODMTHLILRSFKFLOSSLRALROM 212
 DB 181 aonqwldmthlilrsfkflosslralrrom 212

RESULT 2

AAP80269
 ID AAP80269 standard; protein: 212 AA.

AC AAP80269;
 XX
 DT 08-OCT-1990 (first entry)
 XX
 DE Recombinant Interleukin 6.
 XX
 KW IL-6; Interleukin; cancer;
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..27
 FT Modified-site /label=signal peptide
 FT Modified-site 73..75
 FT Modified-site /label-glycosylation site
 FT Modified-site /note="N-linked"
 FT Modified-site 172..174
 FT Modified-site /label-glycosylation site
 FT Modified-site /note="N-linked"

XX WO8800206-A.
 XX
 XX PD 14-JAN-1988.
 XX
 XX PF 07-JUL-1987; 87WO-US01611.
 XX
 XX PR 08-JUL-1986; 86US-0883207.
 XX
 XX (GENE-) GENETICS INST INC.
 XX
 XX PI Clark SC; Wong CG, Schendel P, McCoy J;
 XX
 XX WPI: 1988-021566/03.
 XX
 XX DR N-PSDB: AN80299.
 XX
 XX Prod. of non-glycosylated IL-6 - for use in treatment of deficiency
 XX disorders in haematopoietic cells and in cancer therapy.
 XX
 XX

XX
 PS Disclosure; p; English.
 XX

XX The sequence is encoded by DNA carried by pCSF309 in E.coli MC1061
 CC (ATCC 67153) as an EcoRI insert. This can be excised and used to
 CC construct an expression plasmid for prodn. of IL-6. Bacterially
 CC produced IL-6 is non-glycosylated. It can be used against diseases
 CC caused by decreased levels of either myeloid or lymphoid cells of the
 CC haematopoietic system. It may also be used in conjunction with other
 CC interleukin therapies or as a hybridoma growth factor in culture medium.
 CC See also AAP80270.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 9; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTASGPVAFSLGLLVLPAPAPVPPGDSKDVAAPRROPVLTSSERIDKQIRYI 60
 DB 1 mnsfstasgvpafslgllvlpapapvpvppgdskdvaaprrpvtsseridkqiryi 60
 QY 61 LDGISALRKETCKSNMCESSKEALAEENNLPRMAEKDGCFOGSGFNEETCLVKITIGLL 120
 DB 61 ldgisalrketcksnmcesskealaennlprmaekdgcfgsgfneetclvkiitgll 120
 QY 121 EEFVYLEYIQNRRSESEDOARAVOMSTKVIQFLOKKAKNLDAITPPDPTTNASLITKIQ 180
 DB 121 eefvyleyiqnrrseeseoavomstkvilqflokaknldaitppdpttnaslitkiq 180
 QY 181 AONQWLODMTHLILRSFKFLOSSLRALROM 212
 DB 181 aonqwldmthlilrsfkflosslralrrom 212

RESULT 3

AAP90047
 ID AAP90047 standard; protein: 212 AA.

AC AAP90047;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE pBSF2-L8 sequence.
 XX
 KW pBSF2-L8; pGEM4; clone; Fc epsilon R-gene; IgE; allergy; peptide.
 XX
 PN EP321842-A.
 XX
 XX PD 28-JUN-1989.
 XX
 XX PF 14-DEC-1988; 88EP-0120876.
 XX
 XX PR 22-DEC-1987; 87EP-0100814.
 XX
 XX (OSAU) OSAKA UNIVERSITY.
 XX
 XX PI Kishimoto T, Suemura M, Kikutani H, Barsumian EL, Schneider F-J;
 XX
 XX DR N-PSDB: AAN90131, AAN90132.
 XX
 XX WPI: 1989-186249/26.
 XX
 XX DR N-PSDB: AAN90131, AAN90132.
 XX
 XX PT Cloned gene for eukaryotic expression of Fc epsilon receptor
 XX - for use in treatment and prophylaxis of allergy, esp. asthma.
 XX
 XX PS Disclosure; fig 3; 25pp; English.
 XX
 XX CC The sequence is of pBSF2-L8 including the BSF-2 signal
 XX sequence.
 XX
 XX SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTSAFGVAFSLGLLVLPAAFPAPVPPGDSKDVAAPHROPRTSSERIDKQIRYI 60
 |||||
 Db 1 mnsfstsa fgpvafslglllvlpaa fpa pvp pgsdskdvaaphrqp ltsse rldkqiryi 60
 |||||

QY 61 LDGISALRKETCNKSNMCESSKEALAEENLNLPKMAEKDGCQSGFNETCLVKIITGL 120
 |||||
 Db 61 ldgisalrketcnksnmcesskealaennlnl p kmaekdgc fgs gfn etclvki l tgl 120
 |||||

QY 121 EFVYLEYLQNRFFESSEEQARAVOMSTKVLIOFLQKAKNLDATTDPPTNASILTKIQ 180
 |||||
 Db 121 efeylleylqnrffesseeqaravomstkvliqflqkka nldatt ptp tnasil tklq 180
 |||||

QY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
 |||||
 Db 181 aqnqwlqdm tthlilrsfkeflqsslr alr qm 212
 |||||

RESULT 4

AAP90371
 ID AAP90371 standard; protein; 212 AA.
 XX
 AC AAP90371;
 XX
 DT 01-NOV-1989 (first entry)
 XX
 DE pBSF2-L8.
 XX
 KW FC epsilon receptor; cloned gene; IGE; pBSF2-L8; allergy;
 KW asthma; BSF-2.
 XX
 PN EP321601-A.
 XX
 PD 28-JUN-1989.
 XX
 PF 22-DEC-1987; 87EP-0119080.
 XX
 PR 22-DEC-1987; 87EP-0119080.
 XX
 PA (OSAU) OSAKA UNIVERSITY.
 XX
 PI Kishimoto T, Suemura M, Kikutani H, Barsumian E;
 XX
 DR WPI; 1989-186101/26.
 DR N-PSDB; AAN90134, AAN90135, AAN90136.
 XX
 PT Cloned genes coding for soluble Ige receptor - comprising modified coding
 PT sequence of Fc epsilon receptor gene.
 XX
 PS Disclosure; fig 3; 19pp; English.
 XX
 CC Peptide sequence of pBSF2-L8. See also AAN90134-6.
 CC
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTSAFGVAFSLGLLVLPAAFPAPVPPGDSKDVAAPHROPRTSSERIDKQIRYI 60
 |||||
 Db 1 mnsfstsa fgpvafslglllvlpaa fpa pvp pgsdskdvaaphrqp ltsse rldkqiryi 60
 |||||

QY 61 LDGISALRKETCNKSNMCESSKEALAEENLNLPKMAEKDGCQSGFNETCLVKIITGL 120
 |||||
 Db 61 ldgisalrketcnksnmcesskealaennlnl p kmaekdgc fgs gfn etclvki l tgl 120
 |||||

QY 121 EFVYLEYLQNRFFESSEEQARAVOMSTKVLIOFLQKAKNLDATTDPPTNASILTKIQ 180
 |||||
 Db 121 efeylleylqnrffesseeqaravomstkvliqflqkka nldatt ptp tnasil tklq 180
 |||||

QY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
 |||||
 Db 181 aqnqwlqdm tthlilrsfkeflqsslr alr qm 212
 |||||

QY 121 EFVYLEYLQNRFFESSEEQARAVOMSTKVLIOFLQKAKNLDATTDPPTNASILTKIQ 180
 |||||
 Db 121 efeylleylqnrffesseeqaravomstkvliqflqkka nldatt ptp tnasil tklq 180
 |||||

QY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
 |||||
 Db 181 aqnqwlqdm tthlilrsfkeflqsslr alr qm 212
 |||||

RESULT 5

AAP90436
 ID AAP90436 standard; peptide; 212 AA.
 XX
 AC AAP90436;
 XX
 DT 20-OCT-1989 (first entry)
 XX
 DE Interferon-beta-2.
 XX
 KW Interferon-beta 2; monoclonal antibodies; human;
 KW acute myelogenous leukaemia; breast cancer; bacterial and
 KW parasitic diseases; bone marrow transplants.
 XX
 OS Homo sapiens (human).
 XX
 PN EP326120-A.
 XX
 PD 02-AUG-1989.
 XX
 PF 25-JAN-1989; 89EP-0101295.
 XX
 PR 26-JAN-1988; 88IL-0088376.
 XX
 PA (YEDA) YEDA RESEARCH AND DEV CO LTD.
 XX
 PI Revel M, Rubinstein M, Mory Y, Chen L, Novick D, Michalevicz R;
 XX
 DR WPI; 1989-222084/31.
 DR N-PSDB; AAN90377.
 XX
 PT Monoclonal antibody to human Interferon-beta-2
 PT - produced by hybridoma cell line and useful for leukaemia
 PT treatment etc.
 XX
 PS Disclosure; fig 1; 26 pp; English.
 XX
 CC Interferon-beta-2 (see AAN90377). Used to make
 CC monoclonal antibodies, and in the treatment of the diseases
 CC in KW above.
 CC
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 10; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTSAFGVAFSLGLLVLPAAFPAPVPPGDSKDVAAPHROPRTSSERIDKQIRYI 60
 |||||
 Db 1 mnsfstsa fgpvafslglllvlpaa fpa pvp pgsdskdvaaphrqp ltsse rldkqiryi 60
 |||||

QY 61 LDGISALRKETCNKSNMCESSKEALAEENLNLPKMAEKDGCQSGFNETCLVKIITGL 120
 |||||
 Db 61 ldgisalrketcnksnmcesskealaennlnl p kmaekdgc fgs gfn etclvki l tgl 120
 |||||

QY 121 EFVYLEYLQNRFFESSEEQARAVOMSTKVLIOFLQKAKNLDATTDPPTNASILTKIQ 180
 |||||
 Db 121 efeylleylqnrffesseeqaravomstkvliqflqkka nldatt ptp tnasil tklq 180
 |||||

QY 181 AONQWLQDMTTHLILRSFKEFLQSSLRALROM 212
 |||||
 Db 181 aqnqwlqdm tthlilrsfkeflqsslr alr qm 212
 |||||

```

RESULT 6
ID AAP90469 standard; protein; 212 AA.
XX
XX AAP90469;
AC
XX
XX 01-NOV-1989 (first entry)
DT
XX
XX Interleukin-6.
DE
XX
XX Interleukin-6: lysine-depleted variant.
KM site-directed mutagenesis; human.
XX
XX Homo sapiens.
OS
XX MO8905824-A.
PN
XX
XX 29-JUN-1989.
PD
XX
XX 22-DEC-1988; 88MO-US04633.
PF
XX
XX 23-DEC-1987; 87US-0137043.
PR
XX
XX (GENE ) GENETICS INST INC.
PA
XX
XX Shaw G;
PI
XX
XX MPI: 1989-206594/28.
DR
XX
XX N-PSDB: AAN90255.
DR
XX
XX New lysine depleted variants of polypeptide
PT - opt. modified with hydrophilic residues,
PT biologically active but with altered solubility, stability etc.
PS
XX
XX Disclosure: fig 3; 35pp; English.
CC
XX
XX DNA of interleukin-6 (see corresp. AAN90255). Used in the patent
CC to create lysine depleted variants by site-directed mutagenesis,
CC or synthesis.
XX
XX Sequence 212 AA:

Query Match 100.0%; Score 1071; DB 10; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFCGPVAFSLGLLVLPAAPAPVPYPGEDSKDVAAPRROPULTSSERIDKQIRYI 60
DB 1 mnsfstsa fgpvafslgllvlpaafpapyppgedskdvaaprhprqltsseridkqiryl 60
OY 61 LDGISA LRKRETCNKSNNCESSKEALAEENLNLPKMAEKDGCFOSGFNEETCLVKIITGLL 120
DB 61 ldgisalrketcnksnncsskealaeennlnlpkmaekdgcfcsgfneetclvkiitgll 120
OY 121 EFVYVLEYIQNRRESSPEQARAVOMSTKVILOFLQKAKNLDAITPPDPPTNASLITKIQ 180
DB 121 efvyvleyiqnrresspeqaravomstkviloflqkknldaitppdpptnaslilkq 180
OY 181 AONQMLQDMTTHLILNSFKFELQSSLRALROM 212
DB 181 aonqmqldmtthlilnsfkelfqsslrailrqm 212

```

```

XX
XX Human B-cell differentiation factor gene product.
DE
XX
XX BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
KM
XX
XX Homo sapiens.
OS
XX JP02009388-A.
PN
XX
XX 12-JAN-1990.
PD
XX
XX 08-JUL-1988; 88JP-0170142.
PF
XX
XX 09-MAR-1988; 88JP-0055270.
PR
XX
XX (AJIN ) AJINOMOTO KK.
PA
XX
XX MPI: 1990-055348/08.
DR
XX
XX N-PSDB: AA001763.
DR
XX
XX Physiologically active protein prepn.
PT by transforming plasmid having gene coding physiologically
PT active protein and gene of dihydrofolic acid reductase to hamster
PT ovary etc.
XX
XX Example 3; Fig 6; 12pp; Japanese.
PS
XX
XX Gene may be expressed by transforming a dhfr negative strain of CHO cells
CC with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product
CC is a B-cell differentiating factor.
XX
XX Sequence 212 AA:

Query Match 100.0%; Score 1071; DB 11; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFCGPVAFSLGLLVLPAAPAPVPYPGEDSKDVAAPRROPULTSSERIDKQIRYI 60
DB 1 mnsfstsa fgpvafslgllvlpaafpapyppgedskdvaaprhprqltsseridkqiryl 60
OY 61 LDGISA LRKRETCNKSNNCESSKEALAEENLNLPKMAEKDGCFOSGFNEETCLVKIITGLL 120
DB 61 ldgisalrketcnksnncsskealaeennlnlpkmaekdgcfcsgfneetclvkiitgll 120
OY 121 EFVYVLEYIQNRRESSPEQARAVOMSTKVILOFLQKAKNLDAITPPDPPTNASLITKIQ 180
DB 121 efvyvleyiqnrresspeqaravomstkviloflqkknldaitppdpptnaslilkq 180
OY 181 AONQMLQDMTTHLILNSFKFELQSSLRALROM 212
DB 181 aonqmqldmtthlilnsfkelfqsslrailrqm 212

RESULT 8
ID AAR33430 standard; Protein; 212 AA.
XX
XX AAR33430;
AC
XX
XX 28-JUL-1993 (first entry)
DT
XX
XX IFN-beta-2a.
DE
XX
XX Interferon: IFN; pharmaceutical; inflammation; acute phase response;
KM regulation; cell; proliferation; inhibition; fibroblast; sclerosis;
KM infection; antiviral; antitumor; human; IFN-beta-1; IFN-beta-2;
XX IFN-beta-2a; IFN-beta-2b.
XX
XX Homo sapiens.
OS
XX
XX EP536520-A.
PN

```

XX 14-APR-1993.
 PD
 XX 10-OCT-1986; 86EP-0114478.
 PF
 XX 14-OCT-1985; 85IL-0076714.
 PR 08-MAY-1986; 86US-0860883.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 PI Revel M, Zilberstein A;
 XX
 DR WPI; 1993-118821/15.
 DR N-PSDB; AAQ39582.
 XX
 PT New compsn. contg. human interferon-beta 2A - for treating
 PT inflammation and acute phase response, regulating cell
 PT proliferation, etc.
 PS
 XX Disclosure; Fig 1; 16pp; English.
 CC This sequence represents interferon (IFN)-beta-2a. This protein was
 CC used in the construction of a pharmaceutical composition which was
 CC used for treating inflammation, acute phase response, regulation of
 CC cell proliferation, inhibition of fibroblast proliferation and for
 CC prevention of sclerosis after infection. IFNs are important antiviral
 CC and antitumor proteins produced by the human body. The major species
 CC of IFN produced by human fibroblasts is IFN-beta-1. This is immuno-
 CC logically distinct from IFN-beta-2. Two genes have been found to
 CC encode IFN-beta-2, IFN-beta-2a and IFN-beta-2b.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 14; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTAFGVAVSLGLLVLPAPFAPVPPGSDKVAAPHROPLTSSRIDKQIRYI 60
 DB 1 mnsfstaifgvavslglvlvpafpapyppgsdskvaaphrqpiltsrldkqiryi 60
 QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLPMKAEKDCGFCGSGFNEETCLVKITGLL 120
 DB 61 ldgisalrketcnksnmcesskealaennlpmkaeKdcgfcgsgfneetclvkitgl 120
 QY 121 EFEEYLEYLQNRFESESEBOARAVOMSTKVLIOFLQKAKKNDATTPPTNASILTKIQ 180
 DB 121 efeyyleylqnrfseseeqaravomstkvliqflqkxakndaittpptnaasiltkiq 180
 QY 181 AQNQMLQDMTHLLIRSFKEFLQSSLRALROM 212
 DB 181 aqngwlgdmthllirsfkeflqsslraltlrgm 212

RESULT 9
 AAR34726
 ID AAR34726 standard; protein: 212 AA.
 XX
 AC AAR34726;
 XX
 DT 24-AUG-1993 (first entry)
 XX
 DE Human IL-6 (for modification).
 XX
 KW Interleukin-6; stability; blood; cytokine; BSR-2.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..29
 FT Protein /label= sig-pep
 FT 30..212

FT /label= mat_protein
 XX JP05086099-A.
 FN
 XX 06-APR-1993.
 PD
 XX 31-JUL-1991; 91JP-0191475.
 XX
 PF 31-JUL-1990; 90JP-0204440.
 PR
 XX 31-JUL-1990; 90JP-0204440.
 XX
 PA (TORA) TORAY IND INC.
 PI WPI; 1993-149232/18.
 DR
 DR Modified interleukin-6 derivs. - used to treat platelet-reducing
 PT conditions, thrombocytopenia
 PT
 XX
 PS Claim 1; Page 2; 6pp; Japanese.
 CC A modified interleukin-6 (IL-6) contg. at least 3 sequences of Asn-X-
 CC Thr or Asn-X-Ser, where X is an amino acid other than Pro, is
 CC claimed (no specific sequences, nor the sequence below are given
 CC in the specification 1).
 CC The modified IL-6 can be expected to have higher stability in
 CC blood, higher medical effect and higher absorption in the
 CC objective organ.
 XX
 SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 14; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTAFGVAVSLGLLVLPAPFAPVPPGSDKVAAPHROPLTSSRIDKQIRYI 60
 DB 1 mnsfstaifgvavslglvlvpafpapyppgsdskvaaphrqpiltsrldkqiryi 60
 QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLPMKAEKDCGFCGSGFNEETCLVKITGLL 120
 DB 61 ldgisalrketcnksnmcesskealaennlpmkaeKdcgfcgsgfneetclvkitgl 120
 QY 121 EFEEYLEYLQNRFESESEBOARAVOMSTKVLIOFLQKAKKNDATTPPTNASILTKIQ 180
 DB 121 efeyyleylqnrfseseeqaravomstkvliqflqkxakndaittpptnaasiltkiq 180
 QY 181 AQNQMLQDMTHLLIRSFKEFLQSSLRALROM 212
 DB 181 aqngwlgdmthllirsfkeflqsslraltlrgm 212

RESULT 10
 AAR49041
 ID AAR49041 standard; protein: 212 AA.
 XX
 AC AAR49041;
 XX
 DT 06-SEP-1994 (first entry)
 XX
 DE Human Interleukin-6.
 XX
 KW Interleukin 6; IL-6; thrombocytopenias; surgery.; chemotherapy;
 KW radiation therapy; bone marrow transplantation; cancer therapy;
 KW neoplasia; anti-neoplastic activity.
 XX
 OS Homo sapiens.
 XX
 FN WO9403492-A.
 XX
 PD 17-FEB-1994.
 PD
 PF 01-JUL-1993; 93WO-AU00324.
 XX

PR 06-AUG-1992; 92AU-0003983.
 XX (LUDW-) LUDWIG INST CANCER RES.
 PA (UYME) UNIV MELBOURNE.
 XX
 XX
 PI Simpson RJ, Williams NT;
 XX
 DR WPI: 1994-065607/08.
 DR N-PSDB; AA055973.
 XX
 XX New interleukin-6 variants - capable of stimulating
 PT thrombocytopoiesis while exhibiting low hybridoma growth factor
 PT activity
 PS
 PS Disclosure; Page 33; 46pp; English.
 XX
 CC This sequence is human interleukin-6 (IL-6). IL-6 variants in
 CC the form of non-full length molecules can stimulate, enhance or
 CC facilitate thrombocytopoiesis without the side effects of other IL-6
 CC activites. The IL-6 variants are useful for inducing
 CC thrombocytopoiesis in thrombocytopenic patients following surgery,
 CC chemotherapy, radiation therapy or bone marrow transplantation. The
 CC IL-6 variants may also be useful in cancer therapy where the
 CC fragments express anti-neoplastic activity.
 CC
 SO Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 15; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDYAAPHPQPLTSSERIDQIRYI 60
 |||||
 DB 1 mnsfstsaigpvaafsllivlpafpapypgedskdvaaprgpltsesrdkqiryi 60
 OY 61 LQGISALRKETCKSNMCESSKEALAEENLNLPKMAEKGCQSGNFEETCLVKITGLL 120
 |||||
 DB 61 lqgisalrketcnkmccsskealaennlnlpkmaekdcqsgfneetclvkitgl 120
 OY 121 EFVVYLEYLQNRPESEEOARAVOMSTKVLIQFLOKAKNLDAITPPDPTNASLITKIQ 180
 |||||
 DB 121 efvyleyiqnrpesseegaravqmkvliqfllqkxaknldaitcpdptnaslltkiq 180
 OY 181 AONQWLQDMTTHLILRSFKFLOSSLRALROM 212
 |||||
 DB 181 aqnqwlqdmctthllrsfkfllqsslrailrqm 212

RESULT 11
 AAR49249
 ID AAR49249 standard; Protein: 212 AA.
 XX
 AC AAR49249;
 XX
 DT 15-SEP-1994 (first entry)
 XX
 DE Sequence of human B-cell differentiation factor (BCDF) encoded by
 DE cDNA.
 XX
 KW B-cell differentiation factor; BCDF; antitumour; antilyral;
 KW lymphokine.
 XX
 XX Homo sapiens.
 OS
 XX EP585957-A.
 PN
 PD 09-MAR-1994.
 XX
 PF 06-AUG-1987; 87EP-0111409.
 XX
 PR 06-AUG-1986; 86JP-0184858.
 PR 27-AUG-1986; 86JP-0200433.

PR 18-DEC-1986; 86JP-0302699.
 PR 13-MAY-1987; 87JP-0116332.
 XX
 XX
 PA (AJTN) AJINOMOTO KK.
 PA (KISH/) KISHIMOTO T.
 XX
 PI Akiyama Y, Hirano T, Kishimoto T, Matsui H, Okano A;
 PI Takahara Y;
 XX
 DR WPI: 1994-076278/10.
 DR N-PSDB; AA056265.
 XX
 XX New non-glycosylated human B-cell differentiation factor -
 PT lacking signal sequence and produced in bacteria, useful as
 PT immuno therapeutic for stimulating antibody prodn, treating
 PT cancer etc, also DNA encoding it
 PS
 PS Claim 2; Fig 5; 63pp; English.
 XX
 CC Human T cells transformed by human T cell leukemia virus (HTLV)
 CC produce BCDF which has an activity of 5x10(6) units/ml or more. For
 CC its prepn. RNA is extracted from human T cell line Vr-1 (JPO 50096)
 CC and used to construct a cDNA library. Oligos are constructed from
 CC known N-terminal sequence of BCDF and used to screen the library.
 CC One positive clone, contg. plasmid bpsf2-38, was selected and
 CC sequenced; it includes the codons for an additional 28 AA N-terminal
 CC region. A polypeptide corresp. to AAs 28-212 of AAR49249, and a
 CC recombinant DNA comprising a gene encoding it are claimed.
 CC
 SO Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 15; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4.5e-97;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDYAAPHPQPLTSSERIDQIRYI 60
 |||||
 DB 1 mnsfstsaigpvaafsllivlpafpapypgedskdvaaprgpltsesrdkqiryi 60
 OY 61 LQGISALRKETCKSNMCESSKEALAEENLNLPKMAEKGCQSGNFEETCLVKITGLL 120
 |||||
 DB 61 lqgisalrketcnkmccsskealaennlnlpkmaekdcqsgfneetclvkitgl 120
 OY 121 EFVVYLEYLQNRPESEEOARAVOMSTKVLIQFLOKAKNLDAITPPDPTNASLITKIQ 180
 |||||
 DB 121 efvyleyiqnrpesseegaravqmkvliqfllqkxaknldaitcpdptnaslltkiq 180
 OY 181 AONQWLQDMTTHLILRSFKFLOSSLRALROM 212
 |||||
 DB 181 aqnqwlqdmctthllrsfkfllqsslrailrqm 212

RESULT 12
 AAR72317
 ID AAR72317 standard; Protein: 212 AA.
 XX
 AC AAR72317;
 XX
 DT 14-NOV-1995 (first entry)
 XX
 DE Interferon-beta2A.
 XX
 KW biologically active; interferon-beta2a; IFN-beta2a; cell growth;
 KW terminal differentiation; cancer; inhibit fibroblast proliferation.
 XX
 XX Homo sapiens.
 OS
 XX EP645452-A.
 PN
 PD 29-MAR-1995.
 XX
 PF 10-OCT-1986; 86EP-0114478.

```

XX 14-OCT-1985; 85IL-0076714.
PR 08-MAY-1986; 86US-0860883.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
PI Revel M, Zilberstein A;
XX
XX WPI; 1995-124593/17.
DR N-PSDB; AAO86523.
XX
PT A DNA sequence encoding active interferon beta2A - used in the
PT prod. of the protein for the treatment of cancer, by inhibition
PT of fibroblast proliferation
XX
PS Claim 1; Fig 1; 17pp; English.
XX
CC Biologically active. Interferon-beta2a (IFN-beta2a), including the
CC N-terminus of the mature protein, may be used to influence cell growth
CC and differentiation esp. terminal differentiation of cancer cells and
CC to inhibit fibroblast proliferation preventing sclerosis after
CC infection.
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 16; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSTSAFGVAFSLGLLVLPAPFAPVPFGEDSKDVAAPHQPLTSSRIDKQIRYI 60
DB 1 mnsfstaafgvafts1g11vlpafpavpfgedskdvaaphqpltsseidkqiryi 60
QY 61 LDGTSALRKETCNKSNCESSKEALAEENNLPMKAEKDGCFOSGFNBECTVYITGL 120
DB 61 ldgtsalrketcnksnmcesskealaennnlpmkmaedgcfgs9fneectlvx1lq11 120
QY 121 EFVYLEYLQNRFFESSEBOARAVOMSTKVLIOFLQKRAKNLDAITTPDPTTNASLTKLQ 180
DB 121 efeyyleylqnrffesseegaravqmsckvllqflqkxaknldaittpdptnasl1cklq 180
QY 181 AQNQWLQDMTHTLLIRSFKEFLQSSLRALROM 212
DB 181 aqnqwlqdmthllirsfkelfqsslraltqrm 212

RESULT 13
AAT87816
ID AAT87816 standard; Protein: 212 AA.
XX
AC AAT87816;
XX
DT 24-AUG-2000 (first entry)
XX
DE Human IL-6 protein.
XX
KW NNT-1; human: neurotrophic factor; nootropic; neuroprotective; treatment;
KW anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological;
KW nervous system degeneration; Alzheimer's disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome;
KW Huntington's disease; peripheral neuropathy; neural retina degeneration;
KW retinopathy; immune disorder; hematopoietic disorder; IL-6.
XX
OS Homo sapiens.
XX
PN US6054294-A.
XX
PD 25-APR-2000.
XX
PF 12-DEC-1997; 97US-0988819.
PR 03-FEB-1997; 97US-0792019.

```

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XX (AMGE-) AMGEN INC.
XX
XX Chang M;
XX
XX WPI; 2000-338492/29.
XX
PT New nucleic acids encoding neurotrophic factors useful for stimulating
PT growth of motor or sympathetic neurons for treating neuron cell damage
XX
PS Example VIII; Fig 6; 42pp; English.
XX
CC This invention describes a novel nucleic acid molecule (I) encoding a
CC novel neurotrophic factor (NNT-1) (II) which has nootropic,
CC neuroprotective, anticonvulsant, antiparkinsonian, antidiabetic and
CC ophthalmological activity. (I) is useful for producing NNT-1
CC polypeptides which are useful for treating patients in whom various
CC cells of the central, autonomic, or peripheral nervous system have
CC degenerated and/or have been damaged by congenital disease, trauma,
CC mechanical damage, surgery, stroke, ischemia, infection, metabolic
CC disease, nutritional deficiency, malignancy and/or toxic agents. NNT-1
CC proteins are used to treat diseases like Alzheimer's, Parkinson's,
CC amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's
CC disease, peripheral neuropathy induced by diabetes or other metabolic
CC disorders, and/or dystrophies or degeneration of the neural retina such
CC as retinitis pigmentosa, drug-induced retinopathies, stationary forms of
CC night blindness, progressive cone-rod degeneration, immune disorders and
CC hematopoietic disorders. (I) is effective in treating neurological
CC conditions and promotes neuron regeneration. Neural functions are
CC effectively restored in patients suffering from various neurological
CC disorders. This sequence represents the human IL-6 protein which is
CC described in the method of the invention.
XX
SQ Sequence 212 AA;

Query Match 100.0%; Score 1071; DB 21; Length 212;
Best Local Similarity 100.0%; Pred. No. 4.5e-97;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSSTSAFGVAFSLGLLVLPAPFAPVPFGEDSKDVAAPHQPLTSSRIDKQIRYI 60
DB 1 mnsfstaafgvafts1g11vlpafpavpfgedskdvaaphqpltsseidkqiryi 60
QY 61 LDGTSALRKETCNKSNCESSKEALAEENNLPMKAEKDGCFOSGFNBECTVYITGL 120
DB 61 ldgtsalrketcnksnmcesskealaennnlpmkmaedgcfgs9fneectlvx1lq11 120
QY 121 EFVYLEYLQNRFFESSEBOARAVOMSTKVLIOFLQKRAKNLDAITTPDPTTNASLTKLQ 180
DB 121 efeyyleylqnrffesseegaravqmsckvllqflqkxaknldaittpdptnasl1cklq 180
QY 181 AQNQWLQDMTHTLLIRSFKEFLQSSLRALROM 212
DB 181 aqnqwlqdmthllirsfkelfqsslraltqrm 212

RESULT 14
AAP81156
ID AAP81156 standard; Protein: 212 AA.
XX
AC AAP81156;
XX
DT 15-OCT-1990 (first entry)
XX
DE Human B-cell differentiation factor (BCDF).
XX
KW B-cell differentiation factor; BCDF; cancer; autoimmune.
XX
OS Homo sapiens.
XX
PN EP257406-A.

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```

XX 02-MAR-1988.
PD
XX
XX 06-AUG-1988; 88EP-0111409.
PF
XX
XX 06-AUG-1986; 86JP-0184858.
PR 27-AUG-1986; 86JP-0200433.
PR 18-DEC-1986; 86JP-0302699.
PR 13-MAY-1987; 87JP-0116332.
XX
XX (AJIN ) AJINOMOTO KK.
PA
XX
PI Kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
XX
XX WPI: 1988-057698/09.
DR N-PSDB; AAN81460.
XX
XX Purified polypeptide with B-cell differentiation factor activity -
PT useful in procn. of antibodies for diagnosis and therapy of
PT cancers, infectious diseases etc.
PS
XX Claim 24; Fig 5; 72pp; English.
XX
XX BCDP may be used in the production and repair of B-cells. It is
CC useful in treatment of autoimmune diseases, malignant tumors and
CC may be used to influence B-cells to produce Abs in vitro.
XX
XX Sequence 212 AA;
SQ

```

```

Query Match 99.7%; Score 1068; DB 9; Length 212;
Best Local Similarity 99.5%; Pred. No. 8.8e-97;
Matches 211; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTAGPVAFSIGLLVLPAAFPAPVPPGDSKQVAAPHROPVTSERIDKQIRYI 60
DB 1 mnsfstaigpvaifsigllvlpaaipavppgdskdvaaphrpltsesridkqiryi 60
QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLNPKMAEKDGCFCOSGFNEETCLVKIITGLL 120
DB 61 ldgisalrketcnkmsccskcalaeennlnpkmaekdgcfcgsfneetclvkiitgll 120
QY 121 EREVYLEYVQNRFESSEEDARAVQSTKVLIOFLQKAKNLDATITPDPPTNASLITKIQ 180
DB 121 erevyleyiqnrfesseedqaravqstkvliqflqkknldaitpdpptnaslilkig 180
QY 181 AONOWIQDWTTHLILRSFKEFLOSSLRALROM 212
DB 181 aonowi qdmtlhlilrsfkeflqslralr qm 212

```

```

RESULT 15
AAP82577
ID AAP82577 standard; protein; 212 AA.
XX
XX AAP82577;
AC
XX
XX 05-NOV-1990 (first entry)
DT
XX
XX Leader sequence of of BSF from pBSF2-L8.
DE
XX
XX Lymphocyte; Immunoglobulin E; receptor; IgE; water soluble; allergy;
KM pGEK4; signal sequence.
XX
XX Homo sapiens.
OS
XX
XX EP286700-A.
XX
XX 19-OCT-1988.
PD
XX
XX 11-NOV-1987; 87EP-0105425.
PF
XX
XX 11-NOV-1987; 87EP-0105425.
PR

```

```

XX (OSAU ) OSAKI UNIVERSITY.
PA
XX
XX Kishimoto T, Suemura H, Barsumian, EI;
XX
XX WPI: 1988-308661/44.
DR N-PSDB; AAN80966.
XX
XX Recombinant lymphocyte immunoglobulin E receptor fragments - useful
PT as anti-allergic agents.
PT
XX
XX Disclosure; ; P; English.
XX
XX The plasmid was prep'd. from plasmid pBSF2-38 (Nature 324 73-76 (1986)).
CC A fragment contg. the code for the BSF2 leader sequence was cloned
CC into pGEM4. DNA encoding FC-epsilon R-1 was then ligated into this
CC plasmid to produce a plasmid for the expression of water sol. receptor
CC fragments useful in treating local or systemic IgE-mediated allergic
CC reactions. They are glycosylated and so are biologically active.
XX
XX See also AAP82576.
XX
XX Sequence 212 AA;
SQ

```

```

Query Match 99.4%; Score 1065; DB 9; Length 212;
Best Local Similarity 99.5%; Pred. No. 1.7e-96;
Matches 211; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNSFSTAGPVAFSIGLLVLPAAFPAPVPPGDSKQVAAPHROPVTSERIDKQIRYI 60
DB 1 mnsfstaigpvaifsigllvlpaaipavppgdskdvaaphrpltsesridkqiryi 60
QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLNPKMAEKDGCFCOSGFNEETCLVKIITGLL 120
DB 61 ldgisalrketcnkmsccskcalaeennlnpkmaekdgcfcgsfneetclvkiitgll 120
QY 121 EREVYLEYVQNRFESSEEDARAVQSTKVLIOFLQKAKNLDATITPDPPTNASLITKIQ 180
DB 121 erevyleyiqnrfesseedqaravqstkvliqflqkknldaitpdpptnaslilkig 180
QY 181 AONOWIQDWTTHLILRSFKEFLOSSLRALROM 212
DB 181 aonowi qdmtlhlilrsfkeflqslralr qm 212

```

Search completed: October , 4, 2001, 18:52:09
Job time: 1675 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; Search time 32.27 Seconds

(Without alignments)
135,270 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAFCVAFSLGLL.....LHNSFKETLQSSLRALRQM 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued_Patents_AA:*

2: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*

3: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*

4: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*

5: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*

6: /cgn2_6/prodata/2/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1071	100.0	212	1 US-08-792-019B-9	Sequence 9, Appl1
2	1071	100.0	212	3 US-08-988-819-9	Sequence 9, Appl1
3	1071	100.0	212	4 US-09-016-534-9	Sequence 9, Appl1
4	1071	100.0	212	4 US-08-097-869-7	Sequence 7, Appl1
5	1071	100.0	212	4 US-08-795-473B-6	Sequence 6, Appl1
6	1071	100.0	212	6 5510472-2	Patent No. 5510472
7	955	89.2	188	3 US-09-122-443-12	Sequence 12, Appl1
8	938	87.6	185	1 US-07-632-070B-1	Sequence 1, Appl1
9	938	87.6	185	1 US-07-918-181A-2	Sequence 2, Appl1
10	938	87.6	185	1 US-08-231-575-2	Sequence 2, Appl1
11	938	87.6	185	1 US-08-246-427A-5	Sequence 5, Appl1
12	938	87.6	185	1 US-08-766-620-5	Sequence 5, Appl1
13	938	87.6	185	5 PCT-US93-06928-2	Sequence 2, Appl1
14	938	87.6	185	6 5186931-2	Patent No. 5186931
15	938	87.6	186	1 US-07-632-070B-2	Sequence 2, Appl1
16	938	87.6	186	1 US-07-745-382-20	Sequence 20, Appl1
17	938	87.6	186	1 US-07-921-848-20	Sequence 20, Appl1
18	938	87.6	186	1 US-08-165-301A-20	Sequence 20, Appl1
19	938	87.6	186	3 US-08-469-318-163	Sequence 163, App
20	938	87.6	186	3 US-08-468-609A-163	Sequence 163, App
21	938	87.6	186	4 US-08-810-436-20	Sequence 20, Appl1
22	938	87.6	186	5 PCT-US94-14179-20	Sequence 20, Appl1
23	938	87.6	186	5 PCT-US95-01185-163	Sequence 163, App
24	938	87.6	187	1 US-07-632-070B-3	Sequence 3, Appl1
25	938	87.6	317	3 US-08-469-318-145	Sequence 145, App
26	938	87.6	317	3 US-08-468-609A-145	Sequence 145, App
27	938	87.6	317	5 PCT-US95-01185-145	Sequence 145, App

28	936	87.4	185	1 US-07-918-181A-6	Sequence 6, Appl1
29	936	87.4	185	1 US-08-231-575-6	Sequence 6, Appl1
30	936	87.4	185	5 PCT-US93-06928-6	Sequence 6, Appl1
31	934	87.2	184	1 US-08-567-047-2	Sequence 2, Appl1
32	934	87.2	184	2 US-08-567-048-2	Sequence 2, Appl1
33	934	87.2	184	6 5186931-1	Patent No. 5186931
34	934	87.2	185	2 US-08-716-317-7	Sequence 7, Appl1
35	932	87.0	185	1 US-07-918-181A-4	Sequence 4, Appl1
36	932	87.0	185	1 US-08-231-575-4	Sequence 4, Appl1
37	932	87.0	185	5 PCT-US93-06928-4	Sequence 4, Appl1
38	930	86.8	185	1 US-07-918-181A-8	Sequence 8, Appl1
39	930	86.8	185	1 US-08-231-575-8	Sequence 8, Appl1
40	930	86.8	185	5 PCT-US93-06928-8	Sequence 8, Appl1
41	929	86.7	184	2 US-08-693-182-2	Sequence 2, Appl1
42	929	86.7	184	2 US-09-008-482-2	Sequence 2, Appl1
43	927	86.6	183	1 US-08-009-973-1	Sequence 1, Appl1
44	920	85.9	319	5 PCT-US94-04208-2	Sequence 2, Appl1
45	918	85.7	185	5 PCT-US92-05612-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-08-792-019B-9
; Sequence 9, Application US/08792019B
; Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, MING-SHI
TITLE OF INVENTION: THE NEUTROTROPIC FACTOR NMT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
FEATURE:
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9
Query Match 100.0%; Score 1071; DB 1; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      121 EEEVYLEIYQNFESSEEQARAVOMSTKVLIOFLQKAKNLDATTPDPTNASLITKLQ 180
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QY      181 AONQWLODMTHLILRSFKEFLQSSLRALROM 212
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Db      181 AONQWLODMTHLILRSFKEFLQSSLRALROM 212

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RESULT 2

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US-08-988-819-9
; Sequence 9, Application US/08988819
; Patent No. 6054294
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; TITLE OF INVENTION: NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER DRIVE
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,819
; FILING DATE: 12-DEC-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442A
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
; US-08-988-819-9

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Query Match      100.0%; Score 1071; DB 3; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 LDGISALRKRETCNKSNCMCESSKEALAEENNLNLPKMAEKDGCFCOSGFNEETCLVKIITGILL 120
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QY      121 EEEVYLEIYQNFESSEEQARAVOMSTKVLIOFLQKAKNLDATTPDPTNASLITKLQ 180
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RESULT 3

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US-09-016-534-9
; Sequence 9, Application US/09016534
; Patent No. 6143874
; GENERAL INFORMATION:
; APPLICANT: CHANG, MING-SHI
; APPLICANT: ELLIOTT, GARY S.
; APPLICANT: SARMIENTO, ULLA
; TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: AMGEN INC.
; STREET: ONE AMGEN CENTER
; CITY: THOUSAND OAKS
; STATE: CA
; COUNTRY: USA
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,534
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/792,019
; FILING DATE: 03-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOK, ROBERT R.
; REGISTRATION NUMBER: 31,602
; REFERENCE/DOCKET NUMBER: A-442B
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; FEATURE:
; NAME/KEY: Region
; LOCATION: -30..0
; US-09-016-534-9

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Query Match      100.0%; Score 1071; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      61 LDGISALRKRETCNKSNCMCESSKEALAEENNLNLPKMAEKDGCFCOSGFNEETCLVKIITGILL 120
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Db      61 LDGISALRKRETCNKSNCMCESSKEALAEENNLNLPKMAEKDGCFCOSGFNEETCLVKIITGILL 120
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Db 121 EFEVYLEYLNRRFSESEQARAQVMSTKVLQFQKKAKNDAITTPPTNASILTKLQ 180
QY 181 AONOWLODMTHLILRSKFELQSSLRALROM 212
Db 181 AONOWLODMTHLILRSKFELQSSLRALROM 212

RESULT 4

US-08-097-869-7

; Sequence 7, Application US/08097869
; Patent No. 6204364
; GENERAL INFORMATION:
; APPLICANT: Todaro, George J.
; APPLICANT: Rose, Timothy M.
; TITLE OF INVENTION: HYBRID CYTOKINES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morison & Foerster
; STREET: 545 Middlefield Road, suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,869
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/753,178
; FILING DATE: 30-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24455-20001.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-327-2951
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-097-869-7

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Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LDGISALRKETCNKSNMCESSKEALAEENNLNLPKAEKDGCGFSGFNETCLVYITGLL 120
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Db 121 EFEVYLEYLNRRFSESEQARAQVMSTKVLQFQKKAKNDAITTPPTNASILTKLQ 180
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Db 181 AONOWLODMTHLILRSKFELQSSLRALROM 212

RESULT 5
US-08-795-4738-6
; Sequence 6, Application US/087954738
; Patent No. 6217858
; GENERAL INFORMATION:
; APPLICANT: Galun, Elhan
; APPLICANT: Nahot, Orli
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,473B
; FILING DATE: 11-FEB-1997
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 212 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; US-08-795-4738-6

Query Match 100.0%; Score 1071; DB 4; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTSAFGVAFSLGLLVLPAAFPAPVPPGEDSKVAAAPHROPLTSSERIDKQIRYI 60
Db 1 MNSFSTSAFGVAFSLGLLVLPAAFPAPVPPGEDSKVAAAPHROPLTSSERIDKQIRYI 60
QY 61 LDGISALRKETCNKSNMCESSKEALAEENNLNLPKAEKDGCGFSGFNETCLVYITGLL 120
Db 61 LDGISALRKETCNKSNMCESSKEALAEENNLNLPKAEKDGCGFSGFNETCLVYITGLL 120
QY 121 EFEVYLEYLNRRFSESEQARAQVMSTKVLQFQKKAKNDAITTPPTNASILTKLQ 180
Db 121 EFEVYLEYLNRRFSESEQARAQVMSTKVLQFQKKAKNDAITTPPTNASILTKLQ 180
QY 181 AONOWLODMTHLILRSKFELQSSLRALROM 212
Db 181 AONOWLODMTHLILRSKFELQSSLRALROM 212

RESULT 6
5510472-2
; Patent No. 5510472
; APPLICANT: REVEL, MICHEL, TIOLLAIS, PIERRE
; TITLE OF INVENTION: PRODUCTION OF RECOMBINANT HUMAN
; INTERFERON-BETA2
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/883,633

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; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; APPLICATION NUMBER: 449,447
; FILING DATE: 12-DEC-1989
; APPLICATION NUMBER: 860,883
; FILING DATE: 08-MAY-1986
; APPLICATION NUMBER: 208,925
; FILING DATE: 20-NOV-1980
; SEQ ID NO: 2
; LENGTH: 212
5510472-2

Query Match          100.0%; Score 1071; DB 6; Length 212;
Best Local Similarity 100.0%; Pred. No. 6e-110;
Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNSFSTSAFCVPAFSLGLLLVLPAAFPAPVPPCEDSKDVAAPHRQPLTSSERIDKQIRYI 60
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DB 1 MNSFSTSAFCVPAFSLGLLLVLPAAFPAPVPPCEDSKDVAAPHRQPLTSSERIDKQIRYI 60
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QY 61 LDCISALRKETCKSNMCESSKEALAEENNLNLPKMAEKDCFCOSGFNEETCLVKIITGLL 120
    |||||||
DB 61 LDCISALRKETCKSNMCESSKEALAEENNLNLPKMAEKDCFCOSGFNEETCLVKIITGLL 120
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QY 121 EFVEVLEYLONRFESSEQARAVQMTSKVLIQPLQKAKMLDAITPPPTNASLTLTKIQ 180
    |||||||
DB 121 EFVEVLEYLONRFESSEQARAVQMTSKVLIQPLQKAKMLDAITPPPTNASLTLTKIQ 180
    |||||||

QY 181 AQONQWLODMTHLILRSFKFELQSSLRALKOM 212
    |||||||
DB 181 AQONQWLODMTHLILRSFKFELQSSLRALKOM 212
    |||||||

RESULT 7
US-09-122-443-12
; Sequence 12, Application US/09122443
; Patent No. 6060284
; GENERAL INFORMATION:
; APPLICANT: Bazan, J. Fernando
; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNA Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,443
; FILING DATE: 24-JUL-1998
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,765
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Chung, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0758K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-122-443-12

Query Match          89.2%; Score 955; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 2.9e-97;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AAPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYILDCISALRKETCKSNMCESSKEA 60
    |||||||

QY 85 LAENNLNLPKMAEKDCFCOSGFNEETCLVKIITGLLEFVEVLEYLONRFESSEQARAVQ 144
    |||||||
DB 61 LAENNLNLPKMAEKDCFCOSGFNEETCLVKIITGLLEFVEVLEYLONRFESSEQARAVQ 120
    |||||||

QY 145 MSTKVLIOPLQKAKMLDAITPPPTNASLTLKIQONQWLODMTHLILRSFKFELQSS 204
    |||||||
DB 121 MSTKVLIOPLQKAKMLDAITPPPTNASLTLKIQONQWLODMTHLILRSFKFELQSS 180
    |||||||

QY 205 SLRALKOM 212
    |||||||
DB 181 SLRALKOM 188
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RESULT 8
US-07-632-070B-1
; Sequence 1, Application US/07632070B
; Patent No. 5264209
; GENERAL INFORMATION:
; APPLICANT: Mikayama, Toshihumi
; APPLICANT: APPLICANT: Kadoya, Toshihiko
; APPLICANT: APPLICANT: Kakitani, Makoto
; APPLICANT: APPLICANT: Inoue, Hideo
; TITLE OF INVENTION: Modified hIL-6
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Garsteln,
; STREET: Murray & Bicknell
; STREET: 20 South Clark Street, Suite 2100
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: NBI
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/632,070B
; FILING DATE: 19901221
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-32273
; FILING DATE: 13 FEB 1990
; APPLICATION NUMBER: JP 2-222353
; FILING DATE: 22 AUG 90
; APPLICATION NUMBER: JP 2-250460
; FILING DATE: 21 SEPT 1990
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
US-07-632-070B-1

Query Match          87.6%; Score 938; DB 1; Length 185;

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Best Local Similarity	100.0%	Pred. No.	2,1e-95;
Matches	185;	Conservative	0;
		Mismatches	0;
		Indels	0;
		Gaps	0;

QY	28	APVPGEESKDVAAAPHQPLTSSRIDKQIRYILDGIALRKEFCNKNCESSKELAE	87
Db	1	APVPGEESKDVAAAPHQPLTSSRIDKQIRYILDGIALRKEFCNKNCESSKELAE	60
QY	88	NNLNLPMAEKDGCFQSGFNEETCLVKTIGLLEFEYVLEYLQNRPESSBQAAVQMS	147
Db	61	NNLNLPMAEKDGCFQSGFNEETCLVKTIGLLEFEYVLEYLQNRPESSBQAAVQMS	120
QY	148	KVLIIQFLQKRAKNIDAITTPDPTTNASLTKLQAOONOMLQDMTHLLRSFKEFLOSSLR	207
Db	121	KVLIIQFLQKRAKNIDAITTPDPTTNASLTKLQAOONOMLQDMTHLLRSFKEFLOSSLR	180
QY	208	ALRQM 212	
Db	181	ALRQM 185	

RESULT 9
US-07-918-

Sequence 2, Application US/07918181A
Patent No. 5338833
GENERAL INFORMATION:
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/918,181A
FILING DATE: 23-JUL-1992
CLASSIFICATION: A35
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-918-181A-2

Query Match	87.6%	Score 938	DB 1	Length 185
Best Local Similarity	100.0%	Pred. No. 2	Je-95	
Matches 185	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	28	APVPPEGSDSDVAAPHROPITSSERIDKQIRYLIGLSALRKETCNKSNMCESSKEALAE	87	
Db	1	APVPPEGSDSDVAAPHROPITSSERIDKQIRYLIGLSALRKETCNKSNMCESSKEALAE	60	
QY	88	NNLNLPKMAEKDGFQSGFNEETCDVKIITGLLEFVYLEYLQNNRESSEEDQARAVOMST	147	
Db	61	NNLNLPKMAEKDGFQSGFNEETCDVKIITGLLEFVYLEYLQNNRESSEEDQARAVOMST	120	
QY	148	KVLIOFLQKKAKNDADITTPDPTTNASLLTKLQAOANQIQDMTTHLLRSFKEPFIQSSLR	207	

Db 121 KVLIQFLQKRAKNLDAITTPDPPTNASLTKLQAGQWMLQDMTHILIRSFKEVLQSSLR 180

QY	208	ALROM	212
Db	181	ALROM	185

RESULT 10
US-08-231-575-2

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1      Sequence 2, Application US/08231575
2      Patent No. 5565336
3
4      GENERAL INFORMATION:
5      APPLICANT: Fowlkes, Dana M.
6      TITLE OF INVENTION: C-Terminal IL-6 Mutelins
7      NUMBER OF SEQUENCES: 35
8      CORRESPONDENCE ADDRESS:
9      ADDRESSEE: Imclone Systems Incorporated
10     STREET: 180 Varick Street
11     CITY: New York
12     STATE: New York
13     COUNTRY: United States
14     ZIP: 10014
15
16     COMPUTER READABLE FORM:
17     MEDIUM TYPE: Floppy disk
18     COMPUTER: IBM PC compatible
19     OPERATING SYSTEM: PC-DOS/MS-DOS
20     SOFTWARE: Patent In Release #1.0, Version #1.25
21
22     CURRENT APPLICATION DATA:
23     APPLICATION NUMBER: US/08/231,575
24     FILING DATE: 22-APR-1994
25
26     CLASSIFICATION: 435
27     PRIOR APPLICATION DATA:
28     APPLICATION NUMBER: US 07/918,181
29     FILING DATE: 23-JUL-1992
30
31     ATTORNEY/AGENT INFORMATION:
32     NAME: Sheets, Eric J.
33     REGISTRATION NUMBER: 30,326
34     REFERENCE/DOCKET NUMBER: FOW-2
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: 212-645-1405
37     TELEFAX: 212-645-2054
38
39     INFORMATION FOR SEQ ID NO: 2:
40     SEQUENCE CHARACTERISTICS:
41     LENGTH: 185 amino acids
42     TYPE: amino acid
43     TOPOLOGY: linear
44
45     MOLECULE TYPE: protein
46
47     US-08-231-575-2

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Query Match	87.6%	Score 938	DB 1	Length 185
Best Local Similarly	100.0%	Pred. No.	2.1e-95	
Matches 185; Conservative	0	Mismatches	0	Gaps 0

QY	28	APVPPGEOSKVAA	PHRQPLTSSERIDKQRYITL	DGJISALRKETCN	SNMCESSEKALAE	87
Db	1	APVPPGEOSKVAA	PHRQPLTSSERIDKQRYITL	DGJISALRKETCN	SNMCESSEKALAE	60
QY	88	NNLNLPKAEKDGCF	OSGFNEETCLVKITLGLFE	EYVLEYLQNRFPESSEBO	AAVOMST	147
Db	61	NNLNLPKAEKDGCF	OSGFNEETCLVKITLGLFE	EYVLEYLQNRFPESSEBO	AAVOMST	120
QY	148	KVLIQFLQKAKKNL	DAITTPDPTTNASILLTXLQ	ANOMLQDMTHLLIRSEKFI	QSSLR	207
Db	121	KVLIQFLQKAKKNL	DAITTPDPTTNASILLTXLQ	ANOMLQDMTHLLIRSEKFI	QSSLR	180
QY	208	ALROM	212			
Db	181	ALROM	185			
RESULT	11					

US-08-246-427A-5
; Sequence 5, Application US/08246427A
; Patent No. 5641657
; GENERAL INFORMATION:
; APPLICANT: RUBEN, ET AL.
; TITLE OF INVENTION: Interleukin-6 Splice Variant
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSER: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,427A
; FILING DATE: Submitted herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-246-427A-5

Query Match 87.6%; Score 938; DB 1; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 APVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESSKEALAE 87
DB 1 APVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESSKEALAE 60

QY 88 NNINLPKMAEKDCFCFSGFNEETCLVKIITGILEFEVYLEYLNRRSESEGOARAVOMST 147
DB 61 NNINLPKMAEKDCFCFSGFNEETCLVKIITGILEFEVYLEYLNRRSESEGOARAVOMST 120

QY 148 KVLIOFLQKAKKALDAITPPDPTTNSLTKLQAOQNMQLDMTHILNSFKFLOSSLR 207
DB 121 KVLIOFLQKAKKALDAITPPDPTTNSLTKLQAOQNMQLDMTHILNSFKFLOSSLR 180

QY 208 ALROM 212
DB 181 ALROM 185

RESULT 12
US-08-766-620-5
; Sequence 5, Application US/08766620
; Patent No. 5958400
; GENERAL INFORMATION:
; APPLICANT: RUBEN, ET AL.
; TITLE OF INVENTION: Interleukin-6 Splice Variant

NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSER: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/766,620
; FILING DATE: December 12, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/246,427
; FILING DATE: MAY 19, 1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.C.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-593 (PFI20)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 185 AMINO ACIDS
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; US-08-766-620-5

Query Match 87.6%; Score 938; DB 2; Length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 APVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESSKEALAE 87
DB 1 APVPGEDSKDVAAPHROPITSSERIDKQIRYILDGISALRKETCKNSNMCESSKEALAE 60

QY 88 NNINLPKMAEKDCFCFSGFNEETCLVKIITGILEFEVYLEYLNRRSESEGOARAVOMST 147
DB 61 NNINLPKMAEKDCFCFSGFNEETCLVKIITGILEFEVYLEYLNRRSESEGOARAVOMST 120

QY 148 KVLIOFLQKAKKALDAITPPDPTTNSLTKLQAOQNMQLDMTHILNSFKFLOSSLR 207
DB 121 KVLIOFLQKAKKALDAITPPDPTTNSLTKLQAOQNMQLDMTHILNSFKFLOSSLR 180

QY 208 ALROM 212
DB 181 ALROM 185

RESULT 13
PCT-US93-06928-2
; Sequence 2, Application PC/TUS9306928
; GENERAL INFORMATION:
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Imclone Systems Incorporated
; STREET: 180 Varlick Street
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.

ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19930723
CLASSIFICATION:
PCT/US93/06928
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOM-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 185 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06928-2

Query Match 87.6%; Score 938; DB 5; length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 87
DB 1 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 60
QY 88 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 147
DB 61 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 120
QY 148 KVLIOFLQKRAKNDAITTPPTTNASILTKLQANOMLQDMTHLILRSKFEFLQSSLR 207
DB 121 KVLIOFLQKRAKNDAITTPPTTNASILTKLQANOMLQDMTHLILRSKFEFLQSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

RESULT 14
5186931-2
; PATENT NO. 5186931
; APPLICANT: Kishimoto, Tadami; Hirano, Toshio; Akiyama, Yukio;
; OKANO, AKIRA; Matsui, Hiroshi; Takahara, Yoshiyuki
; TITLE OF INVENTION: COMPOSITION AND METHOD FOR SUPPORTING BONE
; MARROW TRANSPLANTATION
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/366,866
; FILING DATE: 15-JUN-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 81,746
; FILING DATE: 05-AUG-1987
; SEQ ID NO: 2:
; LENGTH: 185
; 5186931-2

Query Match 87.6%; Score 938; DB 6; length 185;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 87
DB 1 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 60
QY 88 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 147
DB 61 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 120
QY 148 KVLIOFLQKRAKNDAITTPPTTNASILTKLQANOMLQDMTHLILRSKFEFLQSSLR 207
DB 121 KVLIOFLQKRAKNDAITTPPTTNASILTKLQANOMLQDMTHLILRSKFEFLQSSLR 180
QY 208 ALROM 212
DB 181 ALROM 185

RESULT 15
US-07-632-070B-2
; Sequence 2, Application US/07632070B
; Patent No. 5264209
; GENERAL INFORMATION:
; APPLICANT: Mikayama, Toshihumi
; APPLICANT: APPLICANT: Kadoya, Toshihiko
; APPLICANT: APPLICANT: Kakitani, Makoto
; APPLICANT: APPLICANT: Inoue, Hideo
; TITLE OF INVENTION: Modified hIL-6
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein,
; ADDRESSEE: Murray & Bicknell
; STREET: 20 South Clark Street, Suite 2100
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
; COMPUTER: IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: NBI
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/632,070B
; FILING DATE: 19901221
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 2-32273
; FILING DATE: 13 FEB 1990
; APPLICATION NUMBER: JP 2-222353
; FILING DATE: 22 AUG 90
; APPLICATION NUMBER: JP 2-250460
; FILING DATE: 21 SEPT 1990
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 186
; TYPE: AMINO ACID
; STRANDEDNESS:
; TOPOLOGY: Linear
; US-07-632-070B-2

Query Match 87.6%; Score 938; DB 1; length 186;
Best Local Similarity 100.0%; Pred. No. 2.1e-95;
Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 87
DB 2 AVPPGSDSKDVAAPHROPPLTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAE 61
QY 88 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 147
DB 62 NNLLPKMAEKDGCFOSGFNEETCLVKIITGILFEVYLEYLQNRPFSSSEBOARAVOMST 121

Fri Oct 5 10:02:12 2001

us-09-230-048-3.rai

Page 8

QY	148	KVLQGFQKKKNNLDATTTPTTNNASLTFRKQAOQOMQLODMFFHLI185FKFQSSLR	207
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QY	208	ALROM	212
Db	182	ALROM	186

Search completed: October 4, 2001, 19:10:32
Job time: 1.63 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Comugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:53 ; Search time 44.98 seconds
(without alignments)
359.026 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAFGPVAFSLGILL.....LILRSFKFRLQSLRALROM 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1071	100.0	212	1	IVHUB2
2	660	61.5	212	1	interleukin-6-prec
3	659	61.5	212	2	interleukin 6 - pi
4	658	61.4	212	2	interleukin 6 - pi
5	567.5	53.0	207	2	interleukin 6 - ca
6	556	51.9	208	1	interleukin-6-prec
7	554	51.7	208	1	interleukin-6- sh
8	435.5	40.7	211	2	interleukin-6-prec
9	420.5	39.3	211	1	interleukin-6-prec
10	123	11.5	201	1	ICMS6
11	99	9.2	208	2	A42247
12	99	9.2	1154	2	A26496
13	96	8.0	1290	2	T15650
14	94.5	8.8	1611	2	A55094
15	94	8.8	253	2	A84743
16	94	8.8	253	2	C84644
17	94	8.8	600	2	T29879
18	92.5	8.6	642	2	A71928
19	91.5	8.5	2269	2	T39607
20	90	8.4	1281	2	T28677
21	89	8.3	725	2	JC5368
22	87.5	8.2	539	2	A47168
23	87.5	8.2	763	2	F72288
24	86.5	8.1	440	1	B86250
25	86.5	8.1	622	2	B70326
26	86	8.0	1927	2	G96703
27	84.5	7.9	1875	2	G64585
28	84	7.8	2319	2	S38173
29	83.5	7.8	623	2	A47004
30					ZPI precursor - mo

30	83	7.7	243	2	F64432	spore coat polysac
31	83	7.7	291	2	S48990	hypothetical prote
32	83	7.7	376	2	T32009	hypothetical prote
33	83	7.7	697	2	T07111	Mar binding filame
34	82.5	7.7	159	2	E81726	conserved hypotet
35	82.5	7.7	313	2	F72366	methionyl-tRNA for
36	82.5	7.7	809	2	S40460	ribosomal protein
37	82.5	7.7	1392	2	A43336	microtubule-vesicl
38	82.5	7.7	1427	2	S22695	reslin - human
39	82	7.7	592	2	A41268	guanine nucleotide
40	82	7.7	685	2	T40364	hypothetical prote
41	82	7.7	1496	2	T19833	hypothetical prote
42	81.5	7.6	932	2	T30099	hypothetical prote
43	81.5	7.6	992	2	T46337	hypothetical prote
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ALIGNMENTS

RESULT 1
IVHUB2
interleukin-6 precursor [validated] - human
N:Alternate names: B-cell differentiation factor; B-cell hybridoma growth factor; B-c
on factor
C:Species: Homo sapiens (man)
C>Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 08-Dec-2000
C:Accession: A32648; A25692; A26966; A33515; A25801; A25921; I52193; I56003; A27601;
R:Yasukawa, K.; Hirano, T.; Watanabe, Y.; Muratani, K.; Matsuda, T.; Nakai, S.; Kishi
EMBO J. 6, 2939-2945, 1987
A:Title: Structure and expression of human B cell stimulatory factor-2 (BSF-2/IL-6) 9
A:Reference number: A32648; MUID:88082664
A:Accession: A32648
A:Molecule type: DNA
A:Residues: 1-212 <YAS>
A:Cross-references: GB:X00081; NID:929494; PIDN:CAA68278.1; PID:929495
A:Note: the authors translated the codon CAG for residue 130 as Glu
R:Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
EMBO J. 5, 2529-2537, 1986
A:Title: Structure and expression of cDNA and genes for human interferon-beta-2, a di
A:Reference number: A91051; MUID:87053818
A:Accession: A25692
A:Molecule type: mRNA
A:Residues: 1-212 <ZIL>
A:Cross-references: GB:X04430; NID:932673; PIDN:CAA28026.1; PID:932674
R:Hirano, T.; Yasukawa, K.; Harada, H.; Yaga, T.; Watanabe, Y.; Matsuda, T.; Kashiwam
I, T.; Kishimoto, T.
Nature 324, 73-76, 1986
A:Title: Complementary DNA for a novel human interleukin (BSF-2) that induces B lymph
A:Reference number: A93387; MUID:87065033
A:Accession: A26966
A:Molecule type: mRNA
A:Residues: 1-212 <HIR>
A:Cross-references: GB:X04602; NID:933849; PIDN:CAA28268.1; PID:933850
R:Touhouchi, N.; Miwa, K.; Karasuyama, H.; Matsui, H.
Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
A:Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization
A:Reference number: A33515; MUID:89391958
A:Accession: A33515
A:Molecule type: mRNA
A:Residues: 1-212 <TOR>
A:Cross-references: GB:M29150; NID:9186349; PIDN:AAA59154.1; PID:9307063
R:Haegeman, G.; Content, J.; Voicikert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
Eur. J. Biochem. 159, 625-632, 1986
A:Title: Structural analysis of the sequence coding for an inducible 26-kDa protein 1
A:Reference number: A25801; MUID:87004683
A:Accession: A25801
A:Molecule type: DNA; mRNA
A:Residues: 1-212 <HAE>
A:Cross-references: GB:X04403
A:Experimental source: Fibroblast
R:May, L.T.; Hellgott, D.C.; Sehgal, P.B.

PROC. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A:Title: Anti-bcr-a-Interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAY>
 A:Cross-references: GB:M14584; NID:9184628; PIDN:AAA52728.1; PID:9306910
 R:Wong, G.C.; Witek-Giennot, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 A:Title: Interleukin 6: Identification as a hematopoietic colony-stimulating factor.
 A:Reference number: 152193; MUID:89193317
 A:Accession: 152193
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:9186351; PIDN:AAA41704.1; PID:9186352
 R:Krenshoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A:Title: Molecular cloning and expression of hybridoma growth factor in *Escherichia coli*
 A:Reference number: 156003; MUID:8808768
 A:Accession: 156003
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BA>
 A:Cross-references: GB:M18403; NID:9184631; PIDN:AAA52729.1; PID:9306911
 R:Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A:Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
 A:Accession: B27601
 A:Molecule type: protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VAZ>
 R:Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990
 A:Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involved
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: protein
 A:Residues: 30-43 <YAM>
 R:Hitano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu, T.
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A:Title: Human beta-cell differentiation factor defined by an anti-peptide antibody and
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: protein
 A:Residues: 29-42 <HIR2>
 R:Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takechi, K.; Hara, T.; Ishikawa, H.; Ar
 Anticancer Res. 11, 961-968, 1991
 A:Title: Purification and characterization of human fibroblast derived differentiation f
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: protein
 A:Residues: 30-42 <MOD>
 A:Experimental source: fibroblast
 R:Min, J.E.; Gernetti, C.; Steinman, R.M.; Graneli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A:Title: Interleukin 6 is the principal cytokine T lymphocyte differentiation factor fo
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R:May, L.T.; Shaw, J.E.; Khanna, A.K.; Zablitsky, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A:Title: Marked cell-type-specific differences in glycosylation of human interleukin-6.
 A:Accession: A48419; MUID:91355644
 A:Reference number: A48419
 A:Molecule type: protein
 A:Residues: 30-37, 'X', 39-40 <MAV2>
 A:Experimental source: FS-4 fibroblasts

A:Note: sequence extracted from NCBI backbone
 A:Note: this 28-30k form contained both N-linked and O-linked carbohydrate; a 25k for
 A:Accession: C48419
 A:Molecule type: protein
 A:Residues: 28-40 <MAV3>
 A:Experimental source: FS-4 fibroblasts
 A:Note: sequence extracted from NCBI backbone (NCBI:63787)
 A:Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R:Orla, T.; Oheda, M.; Hasegawa, M.; Kubonawa, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A:Title: Polypeptide and carbohydrate structure of recombinant human interleukin-6 pr
 A:Reference number: JX0305; MUID:94266765
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R:Clouston, C.L.; Boone, T.C.; Crandall, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A:Title: Disulfide structures of human interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R:Rock, F.L.; Li, X.; Chong, P.; Ide, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A:Title: Roles of disulfide bonds in recombinant human interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: It therefore appears to function as an autocrine factor of cell grow
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB:IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Caeslema's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/Domain: signal sequence #status predicted <SIG>
 F:28-312/Product: interleukin-6, long form #status experimental <MAT>
 F:30-212/Product: interleukin-6, short form #status experimental
 F:72-78,101-111/Disulfide bonds: #status experimental
 F:73/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
 F:166/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
 F:172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	100.0%	Score 1071;	DB 1;	Length 212;
Best Local Similarity	100.0%	Pred. No. 9.3e-80;		
Matches 212;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	1	MNSFSTAFGPVAFSGLLVLPAPFAPVPPEDESKDYAAPHPROPLTSSERIDQIRYI	60	
DB	1	MNSFSTAFGPVAFSGLLVLPAPFAPVPPEDESKDYAAPHPROPLTSSERIDQIRYI	60	
OY	61	LDGISALRKRETCNKSNMCESSKRALAENNLNPKMAEKDGCFOGSENEETCLVKTITGLL	120	
DB	61	LDGISALRKRETCNKSNMCESSKRALAENNLNPKMAEKDGCFOGSENEETCLVKTITGLL	120	
OY	121	EFEEVLEYLQNRRESSEEDARAVOMSTKVLQFLQKAKNLAITPPDTNNSLITKIQ	180	
DB	121	EFEEVLEYLQNRRESSEEDARAVOMSTKVLQFLQKAKNLAITPPDTNNSLITKIQ	180	
OY	181	AONQMDMTTHLLSFKFLOSSRALRM	212	
DB	181	AONQMDMTTHLLSFKFLOSSRALRM	212	

RESULT 2
 T09216
 Interleukin-6 precursor - horse
 C:Species: Equus caballus (domestic horse)
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 23-Jul-1999
 C:Accession: T09216
 R:Swiderski, C.E.; Horohov, D.W.
 submitted to the EMBL Data Library, July 1996
 A:Reference number: 216613
 A:Accession: T09216

QY 181 AONOWLODM-TTHLILRSFKFLOSSLRALRQM 212
::: 11-11::111 111-1
Db 175 CSHIRVAEAINNILLTRLRLDFQLRLRAVRIM 207

```

RESULT/ 6
A56610
Interleukin-6 precursor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A56610; S22162
R:DiCosmans, L.; Cludatz, I.; Cleuter, Y.; Kettmann, R.; Burny, A.
DNA Seq. 2, 411-413, 1992
A:Title: Nucleotide sequence of bovine Interleukin-6 cDNA.
A:Reference number: A56610; MID:93076003
A:Accession: A56610
A:Status: preliminary
A:Molecule type: cDNA
A:Residues: 1-208 <PRO>
A:Cross-references: EMBL:X57317; NID:g2193; PIDD:CA440572.1; PID:g2194
A:Experimental source: BLV induced B cell-1-lymphosarcoma
A:Note: sequence extracted from NCBI backbone (NCBI:118917)
C:Superfamily: Interleukin-6
C:Keywords: cytokine

```

Query Match	51.9%	Score 556;	DB 1;	Length 208;
Best Local Similarity	53.8%	Pred. No. 5.2e-38;		
Matches 113; Conservative	35;	Mismatches 58;	Indels 4;	Gaps 2

[illegible]

RESULT 7
S29549
Interleukin-6 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29549
R:Eberhard, B.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29549
A:Accession: S29549
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-208 <EBR>
A:Cross-references: EMBL:X68723
A:Superfamily: Interleukin-6

Query Match	51.78;	Score 554;	DB 1;	Length 208;
Best Local Similarity	52.98;	Pred. NO. 7.5e-38;		
Matches 111;	Conservative 37;	Mismatches 58;	Indels 4;	Caps 2

```
QY      1 MNSSTSAFPPVAFSGLLLVLEPAFPAPVPPEGDSKDVAAPHKQPLTSSERIDKQIRYI    60C
        |||   ||| : | ||||| : |||   |||   ||| : : |||
Db      1 MNSRFTSASFPLAVSLGILLVMNLSAFPPTPOPLGEDENDTTPSRLLLTTPPEKTALIKHI    60C
```

[illegible]

RESULT 8
A34247
Interleukin-6 precursor - rat
N:Alternate names: IL-6
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
C:Accession: A34247
R:Northeman, W.; Braciak, T.A.; Hattori, M.; Lee, F.; Fey, G.R.
J. Biol. Chem. 264, 16072-16082, 1989
A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-derived cells
A:Reference number: A34247; MUID:89380206
A:Accession: A34247
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-211 <NOR>
A:Cross-references: GB:M26744; NID:g204915; PIDN:AAA7659.1; PID:g204916
A:Superfamily: Interleukin-6
A:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

	Query Match	40.7%	Score 435.5:	DB 2:	Length 211:
	Best Local Similarity	40.8%:	Pred. No. 3.1e-29:		
Matches	87;	Conservative	55;	Mismatches	66;
				Indels	5;
				Gaps	4.
OY	1 MNSFSTAQGVATSLGGLLVLPAAFP-APVPPGGSDKDVAAAPHROPLTSSRIDKQINRY	59			
Dh	1 MKFLSARDFOQVAVF-TGLMLLTATFFPTSOVARCDFETEDT--HNRPVYTTSQVGGLTY	57			
OY	60 ILDGSALRKFTCKNKSNNCSSEKALANNLNILPYMAEKDGFCOSGFNEECILWITIGL	119			
Dh	58 VLREILKEKKELCNGNSCCMSDDLSSTENKLAPETIQNRDGCFOGTGYNOEILIKICSL	117			
OY	120 LEFEVEYTELYONRF-ESSEEQARAVOMSTKYVLIOELQAKKANLDIAITPDPPTNASLTK	178			
Dh	118 LEFRPLYEEFAKNLNODNKDKKARVIQSMTETLVHIFKQEIKDSYKIVLPTPSNMLLMEK	177			
OY	179 LQAQNQMIDMTHLILSLSPKFQLDSSIRALRQ	211			
Dh	178 LESQKEWLRTQTIIOLIKALEEFELKVTRNSTSQ	210			

RECORD 9
 ICM56
 Interleukin-6 precursor - mouse
 N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepatoc
 acyloxa growth factor
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence,revision 30-Jun-1990 #text,change 22-Jun-1999
 C:Accession: A30571; A27610; A30571; S01323; S12103; E34047; A26662; A40466; A60799;
 R:Renaud, O.; Akira, S.; Kamiya, T.; Wong, G.G.; Hirano, T.; Kishimoto, T.
 J. Immunol. 141, 3875-3881, 1988
 A:Title: Genomic structure of the murine IL-6 gene. High degree conservation of poten
 A:Reference number: A30531; MUID:89035525
 A:Accession: A30531
 A:Molecule type: DNA
 A:Residues: 1-211 <TRAN>
 A:Cross-references: GB:NM20572; NID:g198369; PIDN:AA93302.1; PID:g887386
 R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.;
 Eur. J. Immunol. 18, 193-197, 1988
 Eur. J. Immunol. 18, 193-197, 1988
 Description: cDNA cloning of murine Interleukin-6p1; homology with human Interleukin 6.

A:Reference number: A27610.; MUID:88166883
A:Accession: A27610
A:Molecule type: mRNA
A:Residues: 1-211 <YAN>
A:Cross-references: GB:X06203; NID:g52701; PIDN:CAA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justile, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; Cline
J. Immunol. 142, 1372-1376, 1989
A:Title: The murine Il-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383
A:Accession: A30571
A:Molecule type: mRNA
A:Residues: 5-211 <MKOC>
A:Cross-references: GB:M24221; NID:g341131; PIDN:AAA68814.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rudira, M.R.; Van Snick, J.
Eur. J. Biochem. 176, 187-197, 1988
A:Title: Murine hybridoma/Plasmacytoma growth factor. Complete amino-acid sequence and
A:Reference number: S01323; MUID:88329059
A:Accession: S01323
A:Molecule type: protein
A:Residues: 25-166,'X',168-211 <STM>
A:Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 103-A
R:Grenet, H.E.; Fuentes, N.L.; Fuller, G.M.
Nucleic Acids Res. 18, 6455, 1990
A:Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MUID:91057159
A:Accession: S12103
A:Molecule type: mRNA
A:Residues: 1-211 <CORE>
A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CAA38411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J.
Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A:Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleavage
A:Reference number: A90157; MUID:90147691
A:Accession: E34047
A:Molecule type: protein
A:Residues: 66-69,'X',71-75;78-94;128-148 <JMS>
R:Van Snick, J.; Cephas, S.; Vink, A.; Uytendhoe, C.; Coulie, P.G.; Rudira, M.R.; Simp
Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
A:Title: Purification and NH2-terminal amino acid sequence of a T-cell-derived lymphokine
A:Reference number: A26662; MUID:87092311
A:Accession: A26662
A:Molecule type: protein
A:Residues: 25-39,'X',41-42,'X',44-45 <VSN>
R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Kennick, D.; Lee, F.
Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
A:Reference number: A40486; MUID:89017145
A:Accession: A40486
A:Molecule type: mRNA
A:Residues: 1-211 <CHI>
A:Cross-references: GB:J03783; NID:g198367; PIDN:AAA39301.1; PID:g309410
R:Shabo, Y.; Lotem, J.; Rubinstein, M.; Revel, M.; Clark, S.C.; Wolf, S.F.; Kamen, R.; S
Blood 72, 2070-2073, 1988
A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
A:Reference number: A60799; MUID:89062753
A:Accession: A60799
A:Molecule type: protein
A:Residues: 77-98 <SHA>
R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
J. Exp. Med. 171, 965-970, 1990
A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a m
A:Reference number: S10241; MUID:90171860
A:Accession: S10241
A:Molecule type: DNA
A:Status: preliminary
A:Residues: 1-6 <BLA>
A:Cross-references: EMBL:X51457; NID:g49738; PIDN:CAA35824.1; PID:g581860
R:Zhang, J.G.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
Eur. J. Biochem. 211, 53-59, 1993
A:Title: Specific covalent modification of the tyrophophan residues in murine interleukin
A:Reference number: S38254; MUID:94039075
A:Accession: S38254
A:Status: preliminary

A:Molecule type: protein
A:Residues: 38-60;75, 'X', 77-79; 176-203 <H>
C:Genetics:
A:Gene: IL-6
A:Map position: 5
A:Introns: 7/1; 68/3; 106/3; 156/3
C:Superfamily: Interleukin-6
E:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine
F.1-24/Domain: signal sequence; #status predicted <SIG>
F.25-21/Product: Interleukin-6 #status experimental <MAT>

Query Match	39.38;	Score 420.5;	DB 1;	Length 211;
Best Local Similarity	41.88;	Pred. No. 5.1e-27;		
Matches 89;	Conservative 50;	Mismatches 69;	Indels 5;	Gaps 5;

```
Oy      1 MNSFSTAFCGVAFSLGCLLLVLPAAFP-APVPPEEDSKDYAAPHPQPLTSSERIDKOIRY 59
        |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      1 MKFLSARDHFHVAF-LGLMLVTTTAAPPISQVRDFTED-TTPNRP-PVYTTSQVGGLITH 57
```

02 60 ILDGLSALRKETCNKSNMCESSKEALAEENLNLPRKAEKDCFOSGFNEETCLVKIITGL 119

```
QY      120 LEFEYYLEYLONRF-ESSEQRARVOMSTKVLIOFLQAKKANLDIAITPPDPTTNASLTIK 178
        || : |||::: ::::|| : || : | : | : | : ||
DB      118 LEYHSYLEMYKNLNKKDKKARVLQRPDETETLIHFNQEKVDLHKIVLPPIISNALITDK 177
```

```
Oy 179 LQAQNWLODMTTHLILRSFKFLOSSLRALRQ 211
    |:::|::|::|::|::|::|::|::|::|::|
Db 178 LESQKEMLRRTKIQFIKLSLEELKVTILRSTRQ 210
```

RESULT 10
A42247
myelomonocytic growth factor precursor - chicken

C:Accession: A42247; S03633
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1994
C:Species: Gallus gallus (chicken)
R:Sterneck, E.; Blattner, C.; Graf, T.; Leutz, A.

A:Status: preliminary
A:Accession: A42247
A:Reference number: MUID:92195319
A:Title: Structure of the chicken myelomonocytic growth factor gene and sp

A:Residues:1-201 <STE>
A:Note: sequence extracted from NCBI backbone (NCIN:89832, NCIP:89836)
R:Leutz, A.; Damm, K.; Sterneck, E.; Kowenz, E.; Ness, S.; Frank, R.; Gauss
EMBO J 8 175-181 1989

A;Reference number: S03633; MUID:89231616
A;Accession: S03633
A;Molecule type: mRNA

C;Superfamily: interleukin-6
C;Keywords: glycoprotein
F;1-23/Domain: signal sequence #status predicted <SIG>

Query Match	11.5%; Score 123; DB 2; Length 201;
1/1220/201/BRINING PROC. CARBONFUMATE (MAN) (CONTAINING) STATUS PROVIDED	

	Matches	46;	Conservative	40;	Mismatches	93;	Inuits	22;	Gdps
QY	16	LGLLLVLPAAFPAPVPPGEDSKDVAAPHRQPLTSSERIDKQIRYLIDGISALRKETCNKS	75		:::	:	:	: :::	:

Db 8 LALALVLA--PWQALHGAPLAEISGDHDFQLFLKKNLE-FTRKIRGDVAALQRAVCDFE 64

QY 76 MCESSKALAEENNLNLPKMAEKDCFCFSGFNFEETCLVKITGLLEFEVLEYLEYLQNPFES 135

QY 76 NMCESSKEALAE NN L N L P K M A E K D G C F Q S G F N E E T C L Y K I I T G L L E F F E V Y L E Y L Q N R F E S 135

Db 396 EKLHSHSKSVKKLOKOLOK 414

RESULT 14

A84743

probable myosin heavy chain [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001

C:Accession: A84743

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: A84743

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1611 <STO>

A:Cross-references: GB:AE002093; MID:96598338; PIDN:AAF18589.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g33240

A:Map position: 2

C:Superfamily: myosin MYO2; myosin motor domain homology

Query Match 8.8%; Score 94.5; DB 2; Length 1611;

Best Local Similarity 23.3%; Pred. No. 16;

Matches 40; Conservative 33; Mismatches 68; Indels 31; Gaps 5;

QY 34 EDSKDVAAHROPLTSSERIDQIRYILDGIALRKETCNKSNMCSSKEALAEENNLDP 93

Db 917 ODAKTLEKEVEELTSCLELEKQMELEOV-----KTQVEVDLRSLNDMKLQL- 966

QY 94 KMAEKDGFQSGFNEETCLVITITGLLEFVYLYLQNRFSSEEQARAVQMKVLIQF 153

Db 967 -----GETQVTKSEE--ILKIQSALQDMOLEFEELAKELEMTNDLA--AENEQLDLVSS 1017

QY 154 LQKKAKNLDA-----ITPPDPTNASLITKIQAGNQLQDMTHL 193

Db 1018 LQRIKDESDSKYEETSKSEKVEKQEVVIDQGVITIKLEAENQIKALVSTL 1069

RESULT 15

C84644

probable ribonuclease large subunit [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: C84644

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487

A:Accession: C84644

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <STO>

A:Cross-references: GB:AE002093; MID:96623875; PIDN:AAF19216.1; GSPDB:GN00139

C:Genetics:

A:Gene: At2g25100

A:Map position: 2

Query Match 8.8%; Score 94; DB 2; Length 253;

Best Local Similarity 25.6%; Pred. No. 1.9;

Matches 46; Conservative 27; Mismatches 51; Indels 56; Gaps 8;

QY 35 DSKDVAAPHROPLTSSERIDQIRYILDGIALRKETCNKSNMCSSKEALAEENNLDP 94

Db 53 DSKTKKEKRELEYSILKDSLSGMAVDYIDPR-----ELSAKMLAKNKTNLNE 101

QY 95 MAEKDGFQSGFNEETCLVITITGLLEFVYLYLQNRFSSEEQARAVQMKVLIQF 142

Db 102 ISH-----NSAMGLIKRVLDMGVLLTFAVLDVTGDDPKYRIKISERFPS----- 145

QY 143 VQMKTKVLIQF-LQKKAKNLDAITPPDPTNASLITKL---QAQONQLQDMTHLILRSF 198

Db 146 -----IKFVSKKADSLFPI-----VSGASIVAKYTRDRALKEWLVEETGEDINNF 192

Search completed: October 4, 2001, 19:09:55
Job time: 1256 sec

Fri Oct 5 10:02:13 2001

us-09-230-048-3.rpr

Page 8

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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:12:32 ; Search time 27.34 Seconds

(without alignments)
265.624 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAFGVAFSLIALL.....LILRSFKFQLSSLRALROM 212

Scoring table: BIOSUM62

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1071	100.0	212	1 IL6_HUMAN	P05231 homo sapien
2	1033	96.5	212	1 IL6_MACFA	P79341 macaca fasc
3	1032	96.4	212	1 IL6_MACMU	P51494 macaca mula
4	1028	96.0	212	1 IL6_CERTO	P46650 cercocebus
5	660	61.6	208	1 IL6_HORSE	Q95181 equus cabal
6	658	61.4	212	1 IL6_PIG	P26893 sus scrofa
7	657	61.3	209	1 IL6_PHOVI	Q28819 phoca vitul
8	630	58.8	208	1 IL6_FELCA	P41683 felis silve
9	627.5	58.6	207	1 IL6_CANPA	P41323 canis fami
10	620.5	57.9	208	1 IL6_ORCOR	Q28747 orchinus orc
11	564	52.7	205	1 IL6_CAPHI	Q28319 capra bircu
12	559	52.2	208	1 IL6_SHEEP	P29455 ovis aries
13	556	51.9	208	1 IL6_ORCOR	P26892 bos laurus
14	472	44.1	207	1 IL6_MARMO	Q35736 marmota mon
15	435.5	40.7	211	1 IL6_RAT	P20607 rattus norv
16	420.5	39.3	211	1 IL6_MOUSE	P08505 mus musculu
17	345	32.2	125	1 IL6_MUSVI	P41693 mustela vis
18	123	11.5	201	1 MGF_CHICK	P13854 gallus galli
19	99	9.2	208	1 CSF3_MOUSE	P09920 mus musculu
20	96	9.0	1290	1 XCPX_XENLA	P50532 xenopus lae
21	94	8.8	253	1 RNHL_ARATH	Q9566 arabidopsis
22	93.5	8.7	1280	1 MY33_HYDAT	P39922 hydra atten
23	91.5	8.5	1280	1 DYNM_RAT	P28023 rattus norv
24	90	8.4	1281	1 DYNM_MOUSE	Q08788 mus musculu
25	88.5	8.3	512	1 BNAL_HUMAN	Q16515 homo sapien
26	88.5	8.3	512	1 BNAL_RAT	Q62962 rattus norv
27	86.5	8.1	440	1 Y284_AQUAE	Q66638 aquilex aeo
28	84.5	7.9	1875	1 MLPI_YEAST	Q02455 saccharomyc
29	84	7.8	2319	1 F8A_MOUSE	Q06194 mus musculu
30	83	7.7	2291	1 YH09_YEAST	P38882 saccharomyc
31	83	7.7	1270	1 DYNM_HUMAN	Q14203 homo sapien
32	82.5	7.7	313	1 FMTI_THEMA	Q9wy28 thermotoga
33	82.5	7.7	1427	1 REST_HUMAN	P30622 homo sapien

ALIGNMENTS

RESULT ID	IL6_HUMAN	STANDARD:	PRT:	212 AA.
AC	P05231:			
DT	13-AUG-1987 (Rel. 05, Created)			
DT	13-AUG-1987 (Rel. 05, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (B-CELL STIMULATORY FACTOR 2) (BSF-2)			
DE	(INTERFERON BETA-2) (HYBRIDOMA GROWTH FACTOR).			
GN	IL6 OR IFN62.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RX	MEDLINE=8705033; PubMed=3491322.			
RA	Hirano T., Yasukawa K., Harada H., Taga T., Watanabe Y., Matsuda T.,			
RA	Kashiyama S.-I., Nakajima K., Koyama K., Iwamatsu A., Tsunashima S.,			
RA	Sakiyama F., Matsui H., Takahara Y., Taniguchi T., Kishimoto T.;			
RT	"Complementary DNA for a novel human interleukin (BSF-2) that induces			
RT	B lymphocytes to produce immunoglobulin."			
RL	Nature 324:73-76(1986).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88082664; PubMed=3500852;			
RA	Yasukawa K., Hirano T., Watanabe Y., Muratani K., Matsuda T.,			
RA	Nakai S., Kishimoto T.;			
RT	"Structure and expression of human B cell stimulatory factor-2			
RT	(BSF-2/IL-6) gene."			
RL	EMBO J. 6:2939-2945(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87067433; PubMed=3538015;			
RA	May L.T., Heligott D.C., Sehgal P.B.;			
RT	"Anti-beta-interferon antibodies inhibit the increased expression of			
RT	HLA-B7 mRNA in tumor necrosis factor-treated human fibroblasts:			
RT	structural studies of the beta 2 interferon involved."			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:8957-8961(1986).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87053818; PubMed=3023045;			
RA	Zilberstein A., Ruggieri R., Korn J.H., Revel M.;			
RT	"Structure and expression of cDNA and genes for human			
RT	interferon-beta-2, a distinct species inducible by growth-stimulatory			
RT	cytokines."			
RL	EMBO J. 5:2529-2537(1986).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=88088768; PubMed=3320204;			
RA	Brakenhoff J.P.J., de Groot E.R., Evers R.F., Pannkoek H.;			
RA	Aarden L.A.;			
RT	"Molecular cloning and expression of hybridoma growth factor in			
RT	Escherichia coli."			
RL	J. Immunol. 139:4116-4121(1987).			
RN	[6]			

RP SEQUENCE FROM N.A.
 RX MEDLINE-89391958; PubMed-2789513;
 RA Tonouchi N., Miwa K., Katsuyama H., Matsui H.;
 RT "Deletion of 3' untranslated region of human BSF-2 mRNA causes
 RT stabilization of the mRNA and high-level expression in mouse NIH3T3
 RT cells.";
 RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
 RN [17]
 RP SEQUENCE FROM N.A.
 RX TISSUE-Fibroblast;
 RA MEDLINE-87004683; PubMed-3758081;
 RT Haegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
 RA Plets W.;
 RT "Structural analysis of the sequence coding for an inducible 26-kDa
 RT protein in human fibroblasts.";
 RL Eur. J. Biochem. 159:625-632(1986).
 RN [18]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-8919317; PubMed-3266463;
 RA Wong G., Witte-Glanoff J., Hewick R., Clark S., Ogawa M.;
 RT "Interleukin 6: identification as a hematopoietic colony-stimulating
 RT factor.";
 RL Behring Inst. Mitt. 83:40-47(1988).
 RN [19]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93178270; PubMed-1291290;
 RA Chen Q.Y.;
 RT "Stable and efficient expression of human Interleukin-6 cDNA in
 RT mammalian cells after gene transfer.";
 RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
 RN [110]
 RP SEQUENCE OF 30-63.
 RX MEDLINE-88154445; PubMed-3279116;
 RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
 RA Billiau A.;
 RT "Separation and comparison of two monokines with
 RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
 RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
 RL J. Immunol. 140:1534-1541(1988).
 RN [111]
 RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
 RX MEDLINE-95154344; PubMed-7851440;
 RA Breton J., La Flaire A., Bertolero F., Orsini G., Valasina B.,
 RA Zilotto R., de Filippis V., Polverino de Laureto P., Fontana A.;
 RT "Structure, stability and biological properties of a N-terminally
 RT truncated form of recombinant human Interleukin-6 containing a single
 RT disulfide bond.";
 RL Eur. J. Biochem. 227:573-581(1995).
 RN [112]
 RP DISULFIDE BONDS.
 RX MEDLINE-89286115; PubMed-2472117;
 RA Clouston G.L., Boone T.C., Grandall B.C., Mendiaz E.A., Lu H.S.;
 RT "Disulfide structures of human Interleukin-6 are similar to those of
 RT human granulocyte colony stimulating factor.";
 RL Arch. Biochem. Biophys. 272:144-151(1989).
 RN [113]
 RP MUTAGENESIS.
 RX MEDLINE-91243808; PubMed-2037043;
 RA Luetjken C., Kretzgen A., Moeller C., Heinrich P.C., Rose-John S.;
 RT "Evidence for the importance of a positive charge and an
 RT alpha-helical structure of the C-terminus for biological activity of
 RT human IL-6.";
 RL FEBS Lett. 282:265-267(1991).
 RN [114]
 RP STRUCTURE BY NMR.
 RX MEDLINE-96134845; PubMed-8555185;
 RA Nishimura C., Watanabe A., Gouda H., Shimada I., Arata Y.;
 RT "Folding topologies of human Interleukin-6 and its mutants as studied
 RT by NMR spectroscopy.";
 RL Biochemistry 35:273-281(1996).
 RN [115]
 RP STRUCTURE BY NMR.
 RX MEDLINE-97303053; PubMed-9159484;

RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
 RA Cumming D.A.;
 RT "Solution structure of recombinant human Interleukin-6.";
 RL J. Mol. Biol. 268:468-481(1997).
 RN [116]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE-97224126; PubMed-9118960;
 RA Somers W., Stahl M., Seehra J.S.;
 RT "1.9-A crystal structure of Interleukin 6: implications for a novel
 RT mode of receptor dimerization and signaling.";
 RL EMBO J. 16:988-997(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC -----
 DR EMBL: X04430; CAA28026.1; -
 DR EMBL: M14584; AAA52728.1; -
 DR EMBL: X04602; CAA28268.1; -
 DR EMBL: Y00081; CAA68278.1; -
 DR EMBL: M18403; AAA52729.1; -
 DR EMBL: M29150; AAA59154.1; -
 DR EMBL: X04403; CAA27990.1; -
 DR EMBL: X04403; CAA27991.1; -
 DR EMBL: M54894; AAC41704.1; -
 DR EMBL: S56892; AAC13886.1; -
 DR EMBL: A09363; CAA00839.1; -
 DR PIR: A32648; IVH0B2.
 DR PIR: A25921; A25921.
 DR PDB: 1IL6; 04-FEB-98.
 DR PDB: 2IL6; 04-FEB-98.
 DR PDB: 1ALU; 03-JUN-98.
 DR MIM: 147620; -
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSEPMF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR Cytokine; Glycoprotein; Growth factor; signal; 3D-structure.
 KM SIGNAL
 FT SIGNAL 1 29
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78
 FT DISULFID 101 111
 FT CARBOHYD 73 73
 FT MUTAGEN 173 173 N-LINKED (GLYCANC...)
 FT MUTAGEN 185 185 A->V: ALMOST NO LOSS OF ACTIVITY.
 FT MUTAGEN 204 204 W->R: NO LOSS OF ACTIVITY.
 FT MUTAGEN 210 204 S->P: 13% ACTIVITY.
 FT MUTAGEN 212 210 R->K,E,Q,T,A,P: LOSS OF ACTIVITY.
 FT MUTAGEN 212 212 M->T,N,S,R: LOSS OF ACTIVITY.
 SQ SEQUENCE 212 AA: 23718 MW: 1PIEDIFEBI734079 CRC64;
 Query Match 100.0%; Score 1071; DB 1; Length 212;
 Best Local Similarity 100.0%; Pred. No. 4,4e-80;
 Matches 212; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNSFSTSAFGVPAFSGLGLLVLPAPAPAPVPCGDSKDYAAPDRPPLTSSEIRIDKQIRYI 60
 DB 1 MNSFSTSAFGVPAFSGLGLLVLPAPAPAPVPCGDSKDYAAPDRPPLTSSEIRIDKQIRYI 60
 QY 61 LDGISTALRETCNKNMCKSSKKEALAEENLNLPKMAEKGCFCOSGFNETCLVKYITIGLL 120
 DB 61 LDGISTALRETCNKNMCKSSKKEALAEENLNLPKMAEKGCFCOSGFNETCLVKYITIGLL 120

QY 121 EFEVYLEYLNRRFSSSEQAAVOMSTKVLIQFLOKAKKNLDAITTPPTNASLTKLQ 180
 DB 121 EFEVYLEYLNRRFSSSEQAAVOMSTKVLIQFLOKAKKNLDAITTPPTNASLTKLQ 180
 QY 181 AONWLODMTHLILRSKFELQSSSLRALROM 212
 DB 181 AONWLODMTHLILRSKFELQSSSLRALROM 212

RESULT 2

IL6_MACFA STANDARD; PRT; 212 AA.
 ID IL6_MACFA
 AC P79341;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tatsumi M.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC EMBL; AB000554; BAA19148.1; -
 DR HSSP; P05231; 21L6.
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 212 AA; 23654 MW; CF8173FCBF0B0389 CRC64;

Query Match 96.5%; Score 1033; DB 1; Length 212;
 Best Local Similarity 96.7%; Pred. No. 5.3e-77;
 Matches 205; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNSSTSAFGVAFTSLGLLVLPAAFPAPVPPGDSKVAAAPHROPITSSSRIDKQIRYI 60
 DB 1 MNSSTSAFGVAFTSLGLLVLPAAFPAPVPPGDSKVAAAPHROPITSSSRIDKQIRYI 60
 QY 61 LDGISALRKETCNRSNMKESKEALAEENNLNPKMAEKDGCFOGSGFNEETGLVYITGLL 120
 DB 61 LDGISALRKETCNRSNMKESKEALAEENNLNPKMAEKDGCFOGSGFNEETGLVYITGLL 120
 QY 121 EFEVYLEYLNRRFSSSEQAAVOMSTKVLIQFLOKAKKNLDAITTPPTNASLTKLQ 180

DB 121 EFEVYLEYLNRRFSSSEQAAVOMSTKVLIQFLOKAKKNLDAITTPPTNASLTKLQ 180
 QY 181 AONWLODMTHLILRSKFELQSSSLRALROM 212
 DB 181 AONWLODMTHLILRSKFELQSSSLRALROM 212

RESULT 3

IL6_MACMU STANDARD; PRT; 212 AA.
 ID IL6_MACMU
 AC P51494;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 NC NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN-RAC 2;
 RX MEDLINE=96003435; PubMed=7561102;
 RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates.";
 RL J. Immunol. 155:3946-3954(1995).

-1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IL6 PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC EMBL; L26028; AAA99978.1; -
 DR HSSP; P05231; 1ALU.
 DR InterPro: IPR001716; -
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 POTENTIAL.
 FT DISULFID 101 111 POTENTIAL.
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 212 AA; 23728 MW; 4130DFECF0BCAD CRC64;

Query Match 96.4%; Score 1032; DB 1; Length 212;
 Best Local Similarity 96.2%; Pred. No. 6.4e-77;
 Matches 204; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNSSTSAFGVAFTSLGLLVLPAAFPAPVPPGDSKVAAAPHROPITSSSRIDKQIRYI 60
 DB 1 MNSSTSAFGVAFTSLGLLVLPAAFPAPVPPGDSKVAAAPHROPITSSSRIDKQIRYI 60
 QY 61 LDGISALRKETCNRSNMKESKEALAEENNLNPKMAEKDGCFOGSGFNEETGLVYITGLL 120
 DB 61 LDGISALRKETCNRSNMKESKEALAEENNLNPKMAEKDGCFOGSGFNEETGLVYITGLL 120

QY 121 EFEVLEYLONRRESSEEOARAVOMSTKVLOFLOKANKANLDAITTPDPTNASLITKIQ 180
 DB 121 EFEVLEYLONRRESSEEOARAVOMSTKVLOFLOKANKANLDAITTPDPTNASLITKIQ 180
 QY 181 AONOMLODMTHLILRSFKFELLOSSLRALROM 212
 DB 181 AONOMLODMTHLILRSFKFELLOSSLRALROM 212

RESULT 4

IL6_CERTO STANDARD: PRT: 212 AA.
 ID IL6_CERTO
 AC P4650;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Cercopithecus torquatus alys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_Taxid=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FUJ;
 RA VILLINGER F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
 RT "Comparative sequence analysis of cytokine genes from human and
 nonhuman primates."
 RL J. Immunol. 155:3946-3954(1995).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 CC EMBL: I26032; AAA9972.1; -.
 CC DR HSSP: P05231; IALU.
 CC DR InterPro: IPR001716; -.
 CC DR Pfam: PF00489; IL6; 1.
 CC DR PRINTS: PR00433; IL6GCSFMGF.
 CC DR PROSITE: PS00254; INTERLEUKIN-6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; signal.
 CC FT SIGNAL 1 29 BY SIMILARITY.
 CC FT CHAIN 1 29 INTERLEUKIN-6.
 CC FT DISULFID 72 78 POTENTIAL.
 CC FT CARBOHYD 101 111 POTENTIAL.
 CC FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SO SEQUENCE 212 AA; 23668 MW; C73C035226B44B9F CRC64;

Query Match 96.0%; Score 1028; DB 1; Length 212;
 Best Local Similarity 95.8%; Pred. No. 1,4e-76;
 Matches 203; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 MNSFSTSAFGPAVFLGLLLVPAAPVPPGEGDSKDVAAPIHROPJTSSERIDKQIRYI 60
 DB 1 MNSFSTSAFGPAVFLGLLLVPAAPVPPGEGDSKDVAAPIHROPJTSSERIDKQIRYI 60
 QY 61 LDGISAIRKETCNKSNMCKSSKKAALANNLNLPKMAEKDOCCQSGNHEETCLVKTITGILL 120

DB 61 LDGISAIRKETCNKSNMCKSSKKAALANNLNLPKMAEKDOCCQSGNHEETCLVKTITGILL 120
 QY 121 EFEVLEYLONRRESSEEOARAVOMSTKVLOFLOKANKANLDAITTPDPTNASLITKIQ 180
 DB 121 EFEVLEYLONRRESSEEOARAVOMSTKVLOFLOKANKANLDAITTPDPTNASLITKIQ 180
 QY 181 AONOMLODMTHLILRSFKFELLOSSLRALROM 212
 DB 181 AONOMLODMTHLILRSFKFELLOSSLRALROM 212

RESULT 5

IL6_HORSE STANDARD: PRT: 208 AA.
 ID IL6_HORSE
 AC 095181; 019007; 046568;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_Taxid=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Swideraki C.E., Horohov D.W.;
 RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Leuenegger C.M., Huder J.B., von Rechenberg B., Akens M., Auer J.;
 RL Submitted (Jul-1997) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Lai A.C.K.;
 RT "Cloning and expression of equine interleukin-6."
 RT Submitted (Jan-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION. IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U64794; AAB87703.1; -.
 CC DR EMBL: AF005227; AAB6246.1; -.
 CC DR EMBL: AF041975; AAC04574.1; -.
 CC DR HSSP: P05231; IALU.
 CC DR InterPro: IPR001716; -.
 CC DR Pfam: PF00489; IL6; 1.
 CC DR PRINTS: PR00433; IL6GCSFMGF.
 CC DR PROSITE: PS00254; INTERLEUKIN-6; 1.
 CC KW Cytokine; Glycoprotein; Growth factor; signal.
 CC FT SIGNAL 1 27
 CC FT CHAIN 1 28 INTERLEUKIN-6.
 CC FT DISULFID 69 75 BY SIMILARITY.
 CC FT CARBOHYD 98 108 BY SIMILARITY.
 CC FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CONFLICT 4 5 LS -> FF (IN REF. 1).
 CC FT CONFLICT 8 8 T -> A (IN REF. 3).
 CC FT CONFLICT 137 137 I -> V (IN REF. 2).
 CC FT CONFLICT 205 205 V -> I (IN REF. 3).

SO SEQUENCE 208 AA; 23325 MW; A62F4C234056BFB6 CRC64;

Query Match 61.6%; Score 660; DB 1; Length 208;
 Best Local Similarity 61.3%; Pred. No. 8.8e-47;
 Matches 130; Conservative 32; Mismatches 46; Indels 4; Gaps 2;

QY 1 MNSFSTAFSPVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 60
 1 MNSLSTSVTFVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 57
 DB 1 MNSLSTSVTFVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 57

QY 61 LDGIALRKETCNKSNMCKESKEALAEENNLPMKAEKDCGFGSGFNEETCLVITGL 120
 58 LGKISALKNCKNPFCKENSKVLAENNLPMKAEKDCGFGSGFNEETCLVITGL 117
 DB 121 EEEVLEYLONRFESSEQARAVOMSTVLIQIOLKAKKNDATITPTTNASILTKIQ 180
 118 EFOIYLEYLONRFESSEQARAVOMSTVLIQIOLKAKKNDATITPTTNASILTKIQ 176

QY 181 AQONMLODMTHLILRSFKFELQSSLRALROM 212
 177 SQNEMKMTKTHLILRSLEDFLOFSLRARIM 208

RESULT 6
 IL6_PIG STANDARD; PRT: 212 AA.

AC P26893;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91338547; PubMed=1873476;
 RA Richards C., Saklatvala J.;
 RT "Molecular cloning and sequence of porcine interleukin 6 cDNA and
 expression of mRNA in synovial fibroblasts in vitro.";
 RL Cytokine 3:269-276(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92360284; PubMed=1497880;
 RA Mathias J.N., Bixby J.A., Roberts M.R.;
 RT "Expression of interleukin-6 in porcine, ovine, and bovine
 preimplantation conceptuses.";
 RL Mol. Reprod. Dev. 32:324-330(1992).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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CC EMBL; M86722; AAC37333.1; -;
 DR EMBL; M80258; AAC27127.1; -;
 DR HSSP; P05231; IALU.
 DR InterPro; IPR001716; -;
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6GCSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.

DR PROSITE; PS00254; INTERLEUKIN-6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 29 BY SIMILARITY.
 FT CHAIN 30 212 INTERLEUKIN-6.
 FT DISULFID 72 78 BY SIMILARITY.
 FT DISULFID 101 111 BY SIMILARITY.
 FT CONFLICT 30 30 G->E (IN REF. 2).
 SQ SEQUENCE 212 AA; 23880 MW; EF100ED030B6FD0 CRC64;

Query Match 61.4%; Score 658; DB 1; Length 212;
 Best Local Similarity 61.3%; Pred. No. 1.3e-46;
 Matches 130; Conservative 32; Mismatches 50; Indels 0; Gaps 0;

QY 1 MNSFSTAFSPVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 60
 1 MNSLSTSVTFVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 60
 DB 1 MNSLSTSVTFVAFSLGLLVLPAPFAPVPPEGSDKVAAPHROPPLTSSERIDKQIYI 60

QY 61 LDGIALRKETCNKSNMCKESKEALAEENNLPMKAEKDCGFGSGFNEETCLVITGL 120
 61 LGKISAMKCKEKEKESKEVLAENNLPMKAEKDCGFGSGFNEETCLVITGL 120
 DB 121 EEEVLEYLONRFESSEQARAVOMSTVLIQIOLKAKKNDATITPTTNASILTKIQ 180
 121 EFOIYLEYLONRFESSEQARAVOMSTVLIQIOLKAKKNDATITPTTNASILTKIQ 180

QY 181 AQONMLODMTHLILRSFKFELQSSLRALROM 212
 181 SQNEMKMTKTHLILRSLEDFLOFSLRARIM 212

RESULT 7
 IL6_PHOVI STANDARD; PRT: 209 AA.

AC Q28819;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Phoca vitulina (Harbor seal).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Plinnipedia; Phocidae; Phoca.
 OX NCBI_TaxID=9720;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stolt J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 the harbor seal (Phoca vitulina) killer whale (Orcinus orca), and
 Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 or send an email to license@sib-sib.ch).

CC EMBL; I46802; AAB01430.1; -;
 DR HSSP; P05231; 21I6.
 DR InterPro; IPR001716; -;
 DR Pfam; PF00489; IL6; 1.

DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 26 BY SIMILARITY.
 FT CHAIN 27 209 INTERLEUKIN-6.
 FT DISULFID 69 75 BY SIMILARITY.
 FT DISULFID 98 108 BY SIMILARITY.
 SQ SEQUENCE 209 AA; 23483 MW; 75144922E43B48E9 CRC64;

Query Match
 Best Local Similarity 61.3%; Score 657; DB 1; Length 209;
 Matches 127; Conservative 36; Mismatches 44; Indels 0; Gaps 0;

DB 63 ALKREKMDKTKNCEDESKALAEENNLRLPKLAERKDCFGSGFNGECUTLRITTTGLLEFOIH 122
 126 LEYLONFESSESEQARAQVOMSTKVLIOFLQKKAKNLDAITPPDTNASILTKLOANQM 185
 123 LKTIQAVYECNKEDANSVYSTKLIVQMLKKYKSDQEVTPPTPTDTSQALILKADKM 182
 QY 186 LQDTHILIRSFREFLOSSLRALROM 212
 DB 183 LKHITLILRLSEDFLOFSLRAVRIM 209

RESULT 8
 ID IL6_FELCA STANDARD; PRT; 208 AA.
 AC P41683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94162386; PubMed=8117820;
 RA Ohashi T., Matsumoto Y., Watairi T., Gotsuka R., Tsujimoto H.,
 HA Hasegawa A.;
 RT "Molecular cloning of feline interleukin-6 cDNA.";
 RT J. Vet. Med. Sci. 55:941-944(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=94052249; PubMed=8234373;
 RA Bradley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
 RT "Molecular cloning and characterization of a cDNA encoding feline
 interleukin-6.";
 RT Proc. Soc. Biol. Med. 204:301-305(1993).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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CC -----
 DR EMBL: L16914; AAA16620.1; -
 DR EMBL: D13227; BAA02507.1; -
 DR ISSP: P05231; 2IL6.
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCGPWF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 208
 FT DISULFID 68 74 INTERLEUKIN-6.
 FT DISULFID 97 107 BY SIMILARITY.
 FT CONFLICT 2 2 T -> N (IN REF. 2).
 FT CONFLICT 45 45 S -> P (IN REF. 2).
 FT CONFLICT 133 133 E -> K (IN REF. 2).
 FT CONFLICT 173 187 AKLQSGEMLRHHTI -> LSCSHRVAAAHNM (IN
 REF. 2).
 FT CONFLICT 200 201 FS -> LR (IN REF. 2).
 SQ SEQUENCE 208 AA; 23401 MW; 93B4456B2989CA4C CRC64;

Query Match
 Best Local Similarity 58.8%; Score 630; DB 1; Length 208;
 Matches 123; Conservative 34; Mismatches 51; Indels 4; Gaps 1;

DB 1 MNSFTSAFGPAVPSGLILVLPAPAPVPPGSDSDVAAPROPTSSERIDKQIRYI 60
 1 MTFLLTSAPSPPLAFSLQILLVATAPPTPGIAGD-----ATSNRLPLTSADKNEELIKTI 56
 QY 61 LDCISALRKETCNKSNKCESSKEALAEENNLRLPKMAEKDCFGSGFNGECUTLRITTTGL 120
 DB 57 LGRISALKREKMCNKNYKCEDESKALAEENNLRLPKLAERKDCFGSGFNGECUTLRITTTGL 116
 QY 121 EFEVYLEYLONFESSESEQARAQVOMSTKVLIOFLQKKAKNLDAITPPDTNASILTKLO 180
 DB 117 EFGIYLFKLDKYEGBEENKSVYSTNVLLQMLKRRKQKQDEVITIPVPEVGLQAKIO 176
 QY 181 AQOMLQDTHILIRSFREFLOSSLRALROM 212
 DB 177 SQEFMLRHHTIHLTLRLSEDFLOFSLRAVRIM 208

RESULT 9
 ID IL6_CANFA STANDARD; PRT; 207 AA.
 AC P41323;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MONGREL;
 RX MEDLINE=94303924; PubMed=7913298;
 RA Kukiela G.L., Youker K.A., Hawkins H.K., Perrard J.L.,
 RA Michael L.H., Ballantyne C.M., Smith C.W., Etlman M.L.;
 RT "Regulation of ICAM-1 and IL-6 in myocardial ischemia: effect of
 reperfusion.";
 RT Ann. N.Y. Acad. Sci. 723:258-270(1994).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL; U02334; AAA83030.1; -
 DR HSSP; P05231; 21L6.
 DR InterPro; IPR001716; -
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6CSFMGF.
 DR PRINTS; PR00434; INTERLEUKIN6.
 DR PROSITE; PS00254; INTERLEUKIN.6; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 ?
 FT CHAIN 1 ?
 FT DISULFID 67 73
 FT DISULFID 96 106
 SO SEQUENCE 207 AA; 22945 MW; 45540154EAB3CF50 CRC64;

Query Match 58.6%; Score 627.5; DB 1; Length 207;
 Best Local Similarity 59.0%; Pred. No. 3,7e-44;
 Matches 125; Conservative 34; Mismatches 48; Indels 5; Gaps 1;

OY 1 MNSSTSAFGVAFSLGLLIVLPAAPAPVPPEGSDKVAAPHROPITSSRIDKQIRYI 60
 DB 1 MNSLSTS-----AFSLGLLVMTATFPFGPLAGDSKDADNSLPLTSANKVEELIKYI 55
 OY 61 LDGISALRKETCNKSNMCESSKEALAEENNLNLPMAEKDGCFOGSGFNEETCLVYITGL 120
 DB 56 LGKISALRKEMCKDFNCECKEALAEENNLNLPKLECKDGCFOGSGFNEETCLVITGL 115
 OY 121 EPEVYLEYLQNRFFESSEQAAVOMSTKVLQIPLQKAKNIDAITTPPTNASLITKLY 180
 DB 116 EFOHLNLQNGEEDKENVKSVHMTSKILVQMKSKVKNODEVTTPPTDASLQALIQ 175
 OY 181 AONQMDMTHTLILRSFKFLOSLRALROM 212
 DB 176 SQDECVKHTHTLILRSLEDFLOPSLRAVRIM 207

RESULT 10
 IL6_ORCOR
 ID IL6_ORCOR STANDARD; PRT; 205 AA.
 AC Q28747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 OX NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Scott J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.

CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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DR EMBL; L46803; AAB01429.1; -
 DR HSSP; P05231; 1ALU.
 DR InterPro; IPR001716; -
 DR Pfam; PF00489; IL6; 1.
 DR PROSITE; PS00254; INTERLEUKIN.6; 1.
 KM Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1 1
 FT CHAIN 1 21
 FT DISULFID 22 205
 FT DISULFID 64 70
 FT DISULFID 93 103
 FT CARBOHYD 164 164
 SO SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;

Query Match 57.9%; Score 620.5; DB 1; Length 205;
 Best Local Similarity 61.8%; Pred. No. 1.4e-43;
 Matches 123; Conservative 28; Mismatches 47; Indels 1; Gaps 1;

OY 13 AFSGLILVLPAPAPVPPEGSDKVAAPHROPITSSRIDKQIRYI 72
 DB 5 AFSGLILVLPATFPFGPLAGDSKDADNSLPLTSANKVEELIKYI 64
 OY 73 MKNMCESSKEALAEENNLNLPMAEKDGCFOGSGFNEETCLVYITGL 132
 DB 65 EKYDCENSKALAEENNLNLPMAEKDGCFOGSGFNEETCLVITGL 124
 OY 133 FESSEQAAVOMSTKVLQIPLQKAKNIDAITTPPTNASLITKLOAQN-QMLODWT 191
 DB 125 YECDEKALAEVQISKALAOILRQKKNPDEVTPPTNASLNNQSQNDMMKNTKI 184
 OY 192 HILRSFKFLOSLRALR 210
 DB 185 ILILRSLEDFLOPSLRAIR 203

RESULT 11
 IL6_CAPHI
 ID IL6_CAPHI STANDARD; PRT; 208 AA.
 AC Q28319;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97392354; PubMed=9250586;
 RA Takakura H., Mori Y., Tatsumi M.;
 RA "Molecular cloning of caprine IL-6 cDNA and its expression in insect
 RT cells.";
 RL Int. Arch. Allergy Immunol. 113:409-416(1997).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: D86569; BAA13118.1; -.
CC HSSP: P05231; 2116.
CC InterPro: IPR001716; -.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6CSFMGF.
CC DR PROSITE: PS00254; INTERLEUKIN-6; 1.
CC DR CYTOKINE; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 1 298 INTERLEUKIN-6.
CC DISULFID 72 78 BY SIMILARITY.
CC FT DISULFID 101 111 BY SIMILARITY.
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
CC SO SEQUENCE 208 AA; 23423 MW; E92E08BF3E3230A0 CRC64;

Query Match 52.7%; Score 564; DB 1; Length 208;
Best Local Similarity 53.3%; Pred. No. 5.3e-39;
Matches 112; Conservative 37; Mismatches 57; Indels 4; Gaps 2;

OY 1 MNSFSTSAFGPAVAFSLGLLVLPAAFPAPVPGEEDSKDYAAPIHROPLTSSERIDKIRYI 60
DB 1 MNSLFTSAFSPPLAVSLGLLVMTSAFPTPGPLGDEPKNTTSRLTLTPKTEALIKHI 60
OY 61 LDGISAIRKETCNKSNMCKSSKEALAEENNLPKMAEKDGCFCGSGNEETCLVKITGL 120
DB 61 YOKISAIRKEICEKNECKENSKETLAENKLPKMEKKGCGSGFNQAICLITKTAGLL 120
OY 121 EREVLEYIQLNRFESSEEDARAVOMSTKVLIQFLQKAKNLDATTPDPTNSSLTKIQ 180
DB 121 EVOIYIDPLQNEFEQNEQVMELOSSIRLQILKEKTAGL--ITP--PATHTDMLKMQ 176
OY 181 AONQMLDMTTHILRSFKFLOSSLRALR 210
DB 177 SSNEWYKNAKVITIIILRSLENFLOFSLRAIR 206

RESULT 12
IL6_SHEEP
ID IL6_SHEEP STANDARD; PRT; 208 AA.
AC P29455;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE:94041419; PubMed-8225400;
RA Andrews A.E., Barcham G.J., Ashman K., Meeusen E.N.T., Brandon M.R.,
RA Nash A.D.;
RT "Molecular cloning and characterization of a ruminant interleukin-6
RT cDNA."
RL Immunol. Cell Biol. 71:341-348(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Ebrahim B.;
RL Submitted (OCT-1992) to the EMBL/Genbank/DBJ databases.
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL

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CC -----
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X62501; CAA44363.1; -.
CC EMBL: X68723; CAA48662.1; -.
CC EMBL: A19159; CAA01443.1; -.
CC PIR: S29549; S29549.
CC HSSP: P05231; 2116.
CC InterPro: IPR001716; -.
CC Pfam: PF00489; IL6; 1.
CC PRINTS: PR00433; IL6CSFMGF.
CC DR PROSITE: PS00254; INTERLEUKIN-6; 1.
CC DR CYTOKINE; Glycoprotein; Growth factor; Signal.
CC FT SIGNAL 1 29 BY SIMILARITY.
CC CHAIN 1 298 INTERLEUKIN-6.
CC DISULFID 72 78 BY SIMILARITY.
CC FT DISULFID 101 111 BY SIMILARITY.
CC FT CARBOHYD 38 38 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CONFLICT 4 4 L -> R (IN REF. 2).
CC FT CONFLICT 110 110 L -> V (IN REF. 2).
CC FT CONFLICT 171 171 M -> L (IN REF. 2).
CC FT CONFLICT 201 201 S -> R (IN REF. 2).
CC SO SEQUENCE 208 AA; 23446 MW; EEC996C13E3230A0 CRC64;

Query Match 52.2%; Score 559; DB 1; Length 208;
Best Local Similarity 52.9%; Pred. No. 1.3e-38;
Matches 111; Conservative 38; Mismatches 57; Indels 4; Gaps 2;

OY 1 MNSFSTSAFGPAVAFSLGLLVLPAAFPAPVPGEEDSKDYAAPIHROPLTSSERIDKIRYI 60
DB 1 MNSLFTSAFSPPLAVSLGLLVMTSAFPTPGPLGDEPKNTTSRLTLTPKTEALIKHI 60
OY 61 LDGISAIRKETCNKSNMCKSSKEALAEENNLPKMAEKDGCFCGSGNEETCLVKITGL 120
DB 61 YOKISAIRKEICEKNECKENSKETLAENKLPKMEKKGCGSGFNQAICLITKTAGLL 120
OY 121 EREVLEYIQLNRFESSEEDARAVOMSTKVLIQFLQKAKNLDATTPDPTNSSLTKIQ 180
DB 121 EVOIYIDPLQNEFEQNEQVMELOSSIRLQILKEKTAGL--ITP--PATHTDMLKMQ 176
OY 181 AONQMLDMTTHILRSFKFLOSSLRALR 210
DB 177 SSNEWYKNAKVITIIILRSLENFLOFSLRAIR 206

RESULT 13
IL6_BOVIN
ID IL6_BOVIN STANDARD; PRT; 208 AA.
AC P26892;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-HOLSTEIN;
RX MEDLINE-93076003; PubMed-1446077;
RA Drosophila L., Clutts I., Cleuter Y., Kettmann R., Buny A.;
RT "Nucleotide sequence of bovine Interleukin-6 cDNA."
RU DNA Seq. 2:411-413(1992).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X57317; CAA40572.1; -
DR PIR: S22162; S22162.
DR HSP: P05231; 21L6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GSEFMGE.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29
FT CHAIN 30 208
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 38 38
FT SEQUENCE 208 AA; 23758 MW; AOF0009BBA2EC341 CRC64;

Query Match
Best Local Similarity 51.9%; Score 556; DB 1; Length 208;
Matches 113; Conservative 35; Mismatches 58; Indels 4; Gaps 2;

QY 1 MNSSTAFGVAFLGLLPAAPAPVPPGSDSKVAAPHROPITSSERIDKQIRYI 60
DB 1 MNSFTSAFTFPFAVSLGLLVTSAFPPLGDFKNDTPGRLLLTPTEKTELLIKRM 60
QY 61 LDGSAIRKETCNKSNCCESKEALANNLPMKAEKDGCGFSGFNEETLYKITGLL 120
DB 61 VDKISAKKEKCEKNDCESSKELAEKNLPMKMEKDGCGFSGFNOAICLIRTAGLL 120
QY 121 EFEEVLEYLQNRFFESSEAOARAVOMSTRVLIQLOKKAKNIDAITTPPTNASLITKIQ 180
DB 121 EYQIYLDYLONEYEGNGENVADLRKNTIRLQIL-KQKINDLITTP-PAINTDLEKMQ 176
QY 181 AQONQLODMTHLLLRSEKPELQSSLRALR 210
DB 177 SSNEVKNKAKIILIRNLNLEFLQESLRAIR 206

RESULT 14
IL6_MARMO STANDARD; PRT; 207 AA.
ID IL6_MARMO
AC 035736;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RP SEQUENCE FROM N.A.

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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Peripheral blood;
RX MEDLINE-98139533; PubMed-9472070;
RA Lohrengel B., Lu M., Kogendort M.;
RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
RT and IL-6."
RU Immunogenetics 47:332-335(1998).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Y14139; CAA74571.1; -
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GSEFMGE.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 18
FT CHAIN 19 207
FT DISULFID 65 71
FT DISULFID 94 104
FT SEQUENCE 207 AA; 23770 MW; F30D19FB6AD6A600 CRC64;

Query Match
Best Local Similarity 44.1%; Score 472; DB 1; Length 207;
Matches 93; Conservative 41; Mismatches 63; Indels 2; Gaps 1;

QY 15 SLGLLVLPAPAPVPPGSDSKVAAPHROPITSSERIDKQIRYI LDGSAIRKETCNK 74
DB 8 SLGLLVVATAPFAVSEIQLEDGENSVTRNKPTRRASGCTRRQSYLKEVEMKRELCN 67
QY 75 SNCCESKEALANNLPMKAEKDGCGFSGFNEETCYKITGLIEFVLEYLQNRFE 134
DB 68 DETCKSHVAASVNNLPMKMEKDGCGFOTGYNNDCLVITRTSGILEQVLYRYIRNFQ 127
QY 135 SSEQARA--VOMSTKVLIQLOKKAKNIDAITTPPTNASLITKLOAQONQLODMTH 192
DB 128 EGNRRDRAENHOSSKALITELKQEVDPNKTIVPSPANINILAKLESQNDKQVMTMQ 187
QY 193 LILNSPEKPELQSSLRALRQ 211
DB 188 LILNFEDELQFTLRVAVRK 206

RESULT 15
IL6_RAT STANDARD; PRT; 211 AA.
ID IL6_RAT
AC P20607;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6 OR IL-6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RP SEQUENCE FROM N.A.

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RX MEDLINE-89380206; PubMed-2789217;
RA Northemann W., Bracklax T.A., Hattori M., Lee F., Fey G.H.;
RT "Structure of the rat interleukin 6 gene and its expression in
RT macrophage-derived cells.";
RL J. Biol. Chem. 264:16072-16082(1989).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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CC -----
CC
CC EMBL; M26744; AAA7659.1; -
CC EMBL; M26745; AAA41430.1; -
CC PIR; A34247; A34247.
CC HSSP; P05231; 1ALU.
CC InterPro; IPR001716; -
CC Pfam; PF00489; IL6; 1.
CC PRINTS; PR00433; IL6CSFEMGF.
CC PRINTS; PR00434; INTERLEUKIN6.
CC PROSITE; PS00254; INTERLEUKIN_6; 1.
CC CYTOKINE; Growth factor; Glycoprotein; Signal.
CC SIGNAL 1 24 POTENTIAL.
CC FT CHAIN 25 211 INTERLEUKIN-6.
CC FT DISULFID 70 76 BY SIMILARITY.
CC FT DISULFID 99 109 BY SIMILARITY.
SQ SEQUENCE 211 AA; 24357 MW; 17D248A14F96B5C1 CRC64;

Query Match 40.7%; Score 435.5; DB 1; Length 211;
Best Local Similarity 40.8%; Pred. No. 1.4e-28;
Matches 87; Conservative 55; Mismatches 66; Indels 5; Gaps 4;

OY 1 MNSFSTASCPVAFSLGLLVLPAPP-APVPGEDSKDYAAPRQPLTSERIDQIRY 59
DB 1 MKFLSARDQPVAF-LGLMLLTATAPTSOVRKGDTEDTT--HNRPVYTTSOVGGLITY 57
OY 60 ILDGISALRKETCNKSNMCESSKEALANNLNPMAEKDGFSGFNEETCLVKITITGL 119
DB 58 VLREILLEMKRELCNGNSDDALSENNLKPEIQNDGCRGTGYNOEICLKICSGI 117
OY 120 LEFEVYLEYIQNRF-ESSEQARAQVOMSTRVLIQFLQKAKKNDATITPPPTNASLTK 178
DB 118 LEFRFYLEFVKNNLQDNKKDKARVIOSTETLVHIFKOEIKDSYKIVLPTPSNALIMER 177
OY 179 IQAQNQWLDQMTTHLLIRSPKFLQSSLRALRQ 211
DB 178 LESQKEMLRKTKTQLILKALEFLKATYMRSTRQ 210

Search completed: October 4, 2001, 19:12:34
Job time: 269 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 19:11:58 ; Search time 74.43 Seconds
(without alignments)
376.846 Million cell updates/sec

Title: US-09-230-048-3

Perfect score: 1071

Sequence: 1 MNSFSTSAFGVAFSLGILL.....ILNSFKKFLQSLRALRQM 212

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1023	95.5	209	6	097540
2	924	86.3	209	6	097TH3
3	742	69.3	175	6	097TH4
4	664	62.0	160	6	097535
5	643.5	60.1	207	6	09WZ27
6	626	58.5	208	6	09XT80
7	603	56.3	207	6	028403
8	470	43.9	207	11	09JHN3
9	441	41.2	241	6	09MZR1
10	398	37.2	210	11	09WY08
11	277	25.9	118	6	09WZ08
12	277	25.9	118	6	09WZ07
13	260	24.3	118	6	09MZR0
14	257	23.6	118	6	09MZ05
15	253	22.7	94	6	09MZ09
16	243	22.3	101	11	055041
17	225.5	17.1	204	14	040918
18	183	17.1	204	14	040918
19	183	17.1	204	14	098823

20	99	9.2	1154	5	018237	018237 caenorhabd
21	99	9.2	1723	2	09JMX8	09JMX8 helicobacte
22	97	9.1	924	5	015738	015738 dicystocell
23	97	9.1	2756	10	09LJ60	09LJ60 arabidopsis
24	94.5	8.8	1611	10	09SDB6	09SDB6 arabidopsis
25	94	8.8	600	5	021036	021036 caenorhabd
26	94	8.8	1819	2	092LV0	092LV0 helicobacte
27	92.5	8.6	642	3	060129	060129 schistosach
28	91.5	8.5	2269	5	026223	026223 plasmodium
29	89	8.3	725	13	007718	007718 gallus gall
30	89	8.3	980	4	09PK07	09PK07 homo sapien
31	89	8.3	989	4	09P212	09P212 homo sapien
32	88.5	8.3	563	11	055163	055163 ratius norv
33	88.5	8.3	563	11	061203	061203 mus musculu
34	88.5	8.3	623	11	062005	062005 mus musculu
35	87.5	8.2	268	4	09H0J8	09H0J8 homo sapien
36	87.5	8.2	519	4	09H851	09H851 homo sapien
37	87.5	8.2	539	2	09X0N0	09X0N0 thermotoga
38	87.5	8.2	763	10	09SAB1	09SAB1 arabidopsis
39	87.5	8.2	1657	11	09JKE1	09JKE1 mus musculu
40	87	8.1	135	5	09VB51	09VB51 drosophila
41	87	8.1	1588	11	09ESK9	09ESK9 mus musculu
42	86.5	8.1	432	5	09GSC8	09GSC8 plasmodium
43	86.5	8.1	432	5	09GSC5	09GSC5 plasmodium
44	86.5	8.1	432	5	09GSC1	09GSC1 plasmodium
45	86.5	8.1	432	5	09GSB9	09GSB9 plasmodium

ALIGNMENTS

RESULT 1
ID 097540 PRELIMINARY; PRT; 209 AA.
AC 097540;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_Taxid=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patatroyo M.E., Murillo L.A.;
RT *Identification, cloning and sequencing of different interleukin genes
in 4 Aotus species.*
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014510; ADB01536.1; -
DR HSP: P05231; IAU
DR InterPro: IPR003573; -
DR InterPro: IPR003574; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6CSFMGF.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER
FT 209
SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 95.5%; Score 1023; DB 6; Length 209;
Best Local Similarity 96.7%; Pred. No. 6e-84;
Matches 202; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNSFSTSAFGVAFSLGILLVPAAPVPPGDSKDVAAAPHOPITSSRRIDKQIRYI 60
DB 1 MNSFSTSAFGVAFSLGILLVPAAPVPPGDSKDVAAAPHOPITSSRRIDKQIRYI 60
OY 61 LDGISALRKETCNKSNMCESSKEALAEENNLNPKMAEKDGCFOGDFNETCLVRIITGLL 120

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DB 61 LOGISALRKETCKSNMCCSSKEALAEENNUNLPKMAEKDCCFOSGNEETCLVKITITGL 120
OY 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 180
DB 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 180
OY 181 AONQMLQDMTHILIRSFKEFIQSSIRAL 209
DB 181 AONQMLQDMTHILIRSFKEFIQSSIRAL 209

RESULT 2
OYTH3 PRELIMINARY: PRT: 209 AA.
AC OYTH3:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus lemurinus (Northern gray-necked night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=43147;
RN 11
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT "Aotus lemurinus gene for IL-6."
RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF093323; AAF21298.1; -.
DR HSSP; P05231; 1ALU.
DR InterPro; IPR003573; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT 209
SQ SEQUENCE 209 AA; 23115 MW; AOA3DFAAHF560CC CRC64;

Query Match 86.3%; Score 924; DB 6; Length 209;
Best Local Similarity 89.0%; Pred. No. 4.3e-59;
Matches 186; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

OY 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
DB 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
OY 61 LOGISALRKETCKSNMCCSSKEALAEENNUNLPKMAEKDCCFOSGNEETCLVKITITGL 120
DB 61 LOGISALRKETCKSNMCCSSKEALAEENNUNLPKMAEKDCCFOSGNEETCLVKITITGL 120
OY 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 180
DB 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 180
OY 181 AONQMLQDMTHILIRSFKEFIQSSIRAL 209
DB 181 AONQMLQDMTHILIRSFKEFIQSSIRAL 209

RESULT 3
OYTH4 PRELIMINARY: PRT: 175 AA.
AC OYTH4:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)

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DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nigriceps (black-headed night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN 11
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
RA Patarroyo M.E.;
RT "Aotus nigriceps gene for IL-6."
RT Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF093322; AAF21297.1; -.
DR HSSP; P05231; 1ALU.
DR InterPro; IPR002069; -.
DR InterPro; IPR003573; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00434; IL6GCSFMGF.
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT 175
SQ SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match 69.3%; Score 742; DB 6; Length 175;
Best Local Similarity 87.6%; Pred. No. 6.6e-59;
Matches 148; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

OY 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
DB 1 MNSFSTSAFPAVAFSLGLLVLPAPFAPVPGEDSKDVAAPHRQPLTSSERIDKQIRYI 60
OY 61 LOGISALRKETCKSNMCCSSKEALAEENNUNLPKMAEKDCCFOSGNEETCLVKITITGL 120
DB 61 LOGISALRKETCKSNMCCSSKEALAEENNUNLPKMAEKDCCFOSGNEETCLVKITITGL 120
OY 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 169
DB 121 EFEVYLEYLNRRSESEEOARAVOMSTKVLIOFLQKAKNLDAITPPDPTNASTLTGL 169

RESULT 4
OYTH3 PRELIMINARY: PRT: 160 AA.
AC OYTH3:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN 11
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
RA "Identification, cloning and sequencing of different Interleukin genes
in 4 Aotus species."
RT Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF014505; AAD01531.1; -.
DR HSSP; P05231; IL6.
DR InterPro; IPR003573; -.
DR InterPro; IPR003574; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFMGF.
DR PROSITE; PS00254; INTERLEUKIN6.
DR SMART; SM00126; IL6; 1.
FT NON_TER 1
FT 160

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SQ SEQUENCE 160 AA; 1785 MW; 07A021338650A46D CRC64;

Query Match	Score	DB	Length
62.08;	664;	6;	160;
88.58;	704;	5;	70-83;

Matches	131;	Conservative	10;	Mismatches.	7
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Matches 131; Conservative 10; Mismatches. 7; Indels 0; Gaps 0;

[illegible]

RESULT	5
COVER	

171W60

PRELIMINARY; PRT; 207 AA.

DT 01-OCT-2000 (TREMBLref. 15, Created)
DT 01-OCT-2000 (TREMBLref. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLref. 16, Last annotation update)
DE INTERLEUKIN-6.
GN IL-6.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxId=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Youn H.-Y., Shin I.-S.,
RT "Canine IL-6 mRNA".
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF275196; AAF86275.1; -.
DR InterPro; IPR003573; -.
DR InterPro; IPR003574; -.
DR Pfam; PF00489; IL6; 1.
DR PRINTS; PRO0433; IL6GCSFMGF.
DR PRINTS; PRO0434; INTERLEUKIN6.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR SMART; SM00126; IL6; 1.
SQ SEQUENCE 207 AA; 23042 MW; 45541AE011C80F50 CRC64;

Query Match	Score	DB	Length
60.18	643.5	DB 6	207

Best Local Similarity 59.9%; Pred. No. 5.2e-50;

Matches 127; Conservative 33; Mismatches 47; Indels 5; Gaps 1.

[illegible]

RESULT 6

09X180

PRELIMINARY; PRT; 208 AA.

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AC      O9XT80;
DT      01-NOV-1999 (TREMBLrel. 12, Created)
DT      01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT      01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE      INTERLEUKIN 6 PRECURSOR.
OS      Delphinapterus leucas (Beluga Whale).
OC      Eukaryota; Metazoa; Chordata; Cranilia; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC      Monodontidae; Delphinapterus.
OX      NCBI_TaxID=9749;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT      "Molecular cloning and phylogenetic analysis of beluga whale
RL      (Delphinapterus leucas) interleukin 6."
RL      submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF076643; AAD42929.1; -.
DR      HSSP; P05231; 1ALU.
DR      InterPro; IPR003573; -.
DR      InterPro; IPR003574; -.
DR      Pfam; PF00489; IL6; 1.
DR      PRINTS; PR00433; IL6GCSFMGF.
DR      PRINTS; PR00434; INTERLEUKIN6.
DR      PROSITE; PS00254; INTERLEUKIN_6; 1.
DR      SMART; SM00126; IL6; 1.
SO      SEQUENCE     208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

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Query Match	Score	DB	Length
58.58;	626;	6;	208;

Best Local Similarity 00.26; PREU. NO. 1.9e-46;
Matches 137; Corresponding 38; Mismatches 99

Matches	127	conservative	26	mismatches	50	indels	6	gaps	2
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[illegible]

RESULT

Q28403

Q28403	PRELIMINARY;	207 AA
Q28403	PRT;	

DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Eukarya, Lutris (Sea otter).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Emhydra.
OX NCBI_TaxID=34882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; PubMed=8575817;
RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
RA Stott J.L., Fierick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (*Phoca vitulina*), killer whale (*Orcinus orca*), and
RT Southern sea otter (*Emhydra lutris nereis*).";
RL Immunogenetics 43:190-195(1996).
DR EMBL, E46804; AAB01428.1; -.
DR HSSP; P05231; IIL6.

DR InterPro: IP0003573; -
 DR InterPro: IP0003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 207 AA: 23527 MW: 729EDCD91136D8B CRC64:

Query Match 56.3%; Score 603; DB 6; Length 207;
 Best Local Similarity 57.7%; Pred. No. 2,2e-46;

Matches 120; Conservative 37; Mismatches 49; Indels 2; Gaps 1;

OY 5 STSAGPVAFSLGLLVLPAAFPAPVPPEGDSKDVAAPHROPLTSSERIDKOIRYLIDGI 64
 DB 2 STSAGPVAFSLGLLVLPAAFPAPVPPEGDSKDVAAPHROPLTSSERIDKOIRYLIDGI 61
 OY 65 SALRKETCKNSKNCESSEKALAEENNLPRMAEKDCFGSGFNEETCLVYITGLLEFEV 124
 DB 62 SALRNEMCKRYNCEDESKVEALENNINLPKLAEKDRCFQSRFQGTCLIRITTTGLQEFQI 121
 OY 125 YLEYLONRESSEEQARAVQMSKVLIOFLQKKAKNLDAITTPDPTNASLTKLQAOQD 184
 DB 122 HLKYLESNNEGKNDNHSYISTKILLQTL--RPMQIEVTPDPTDASLQALFKSQDK 179
 OY 185 WLQDMTHLILNSFKFLOSSLRALRQW 212
 DB 180 WLKHTTHILRLRLEDFLOPSLRATRM 207

RESULT 8
 ID O9JHH3 PRELIMINARY; PRT: 207 AA.
 AC O9JHH3
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Scurinae;
 OC Marmota.
 OX NCBI_TaxID=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PERIPHERAL BLOOD;
 RA LI D.H., Cullen J.M.;
 RT "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis."
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA LI D.H., Cullen J.M.;
 RT "Gene Structure of the Woodchuck Interleukin-6."
 RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF012908; AAF34861.1; -
 DR EMBL: AF122896; AAF28873.1; -
 DR InterPro: IP0003573; -
 DR InterPro: IP0003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA: 23645 MW: AD2F46D450E13470 CRC64:

Query Match 43.9%; Score 470; DB 11; Length 207;
 Best Local Similarity 46.7%; Pred. No. 1.7e-34;
 Matches 93; Conservative 40; Mismatches 64; Indels 2; Gaps 1;

OY 15 SLGLLVLPAAFPAPVPPEGDSKDVAAPHROPLTSSERIDKOIRYLIDGIALRKETCKN 74
 DB 8 SLGLLVLPAAFPAPVLEQEDGNSVTNRKPTRASSGKAGQSYLKEVFEKRLCKN 67
 OY 75 SNKCESSKALAEENNLPRMAEKDCFGSGFNEETCLVYITGLLEFEYLYLQNRPE 134
 DB 68 DETCISHVAVSENNINLPKMAEKDCFGTGVNRDCLVITISGLLEFQVYLYIRNKFQ 127
 OY 135 SSEEQARA--VQMSKVLIOFLQKKAKNLDAITTPDPTNASLTKLQAOQDLODMTH 192
 DB 128 EGNRRRAEHVQFSSKALFELKQEVKDPKIVFPSPYANINLAKLESQNDQKVMTQ 187
 OY 193 LILRSFKFLOSSLRALRQ 211
 DB 188 LILSNFEDFLQTLRAVRK 206

RESULT 9
 ID O9MZRI PRELIMINARY; PRT: 241 AA.
 AC O9MZRI
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN 6.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN, LYMPH NODE;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 European rabbit (Oryctolagus cuniculus).";
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169176; AAF86660.1; -
 DR InterPro: IP0003573; -
 DR InterPro: IP0003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSPMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 241 AA: 27021 MW: 781D323692C3BE97 CRC64:

Query Match 41.2%; Score 441; DB 6; Length 241;
 Best Local Similarity 47.2%; Pred. No. 8.2e-32;
 Matches 102; Conservative 30; Mismatches 78; Indels 6; Gaps 4;

OY 1 MNSFSTSAF--GPVAFSLGLLVLPAAFPAPVPPEGDSKDVAAPHROPLTSSERIDKOIR 58
 DB 1 MNSF-TSALRPGPLGCSLLLVAVATFPTSAFVRDSSTKASPD-
 OY 59 YLIDGIALRKETCKNSKNCESSEKALAEENNLPRMAEKDCFGSGFNEETCLVYITGL 118
 DB 59 SLLETKELRKEMCHQDVCMNRKALAVNIALPRLIEDGCFPAVANNETCLRTSG 118
 OY 119 LLEFEYLYLQNRPESEEQARA--VQMSKVLIOFLQKKAKNLDAITTPDPTNASL 176
 DB 119 LMEFMYLEHLQAKFSDSEENRVSVNLNIOHLIKTLAPKVNINEEATLPAVAVSIM 178
 OY 177 TKLQAOQDLODMTHLILRSFKFLOSSLRALRQW 212
 DB 179 ENLQQRNQLKTTTHITLIGLNFLEFLRAVDLM 214

RESULT 10
 ID O9WY08 PRELIMINARY; PRT: 210 AA.
 AC O9WY08;


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DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Syllilagus auduboni1 (desert cottontail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Syllilagus.
OX NCBI_TaxID=30581;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169177; AAF86661.1; -
DR InterPro: IPR003573; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA: 13763 MW: 9DDDEG812ED31049 CRC64;

Query Match 24.3%; Score 260; DB 6; Length 118;
Best Local Similarity 45.8%; Pred. No. 5.4e-16;
Matches 54; Conservative 21; Mismatches 41; Indels 2; Gaps 1;

OY 97 EKDGCQSGFNEETCLVKITITGLFEVYLYQNRFSSSEQARA--VOMSTKYLIOPL 154
DB 1 EEDGCFPLAANHETCLRTSGLEFQWYLEHQAQFRSEENTRVSMLKNNRHILNTL 60
OY 155 OKKAKNLDAITTPDPTNNSLTCLKAQNOMQLDMTHILRSFKEFLQSSIRALROM 212
DB 61 RKVKVNFEGVTLKPAIVASLMENLQOKDMKTTIHIFILGLDIFLOFTLRSVRLM 118

RESULT 14
OQM205 PRELIMINARY: PRT: 145 AA.
AC OQM205:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, LYMPH NODES;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169184; AAF74824.1; -
DR InterPro: IPR003573; -
DR InterPro: IPR003574; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 145 AA: 16526 MW: 9679314A2AD3F01C CRC64;

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Query Match 24.0%; Score 257; DB 6; Length 145;
Best Local Similarity 45.8%; Pred. No. 1.3e-15;
Matches 54; Conservative 19; Mismatches 43; Indels 2; Gaps 1;

OY 97 EKDGCQSGFNEETCLVKITITGLFEVYLYQNRFSSSEQARA--VOMSTKYLIOPL 154
DB 1 EEDGCFPLAANHETCLRTSGLEFQWYLEHQAQFRSEENTRVSMLKNNRHILNTL 60
OY 155 OKKAKNLDAITTPDPTNNSLTCLKAQNOMQLDMTHILRSFKEFLQSSIRALROM 212
DB 61 RKVKVNFEGVTLKPAIVASLMENLQOKDMKTTIHIFILGLDIFLOFTLRSVRLM 118

RESULT 15
OQM209 PRELIMINARY: PRT: 118 AA.
AC OQM209:
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-MAR-2001 (TREMBlrel. 16, last annotation update)
DE INTERLEUKIN 6 (FRAGMENT).
GN IL-6.
OS Syllilagus nuttallii (mountain cottontail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Syllilagus.
OX NCBI_TaxID=50378;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=OVARY;
RX MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RL European rabbit (Oryctolagus cuniculus).";
EMBL: AF169178; AAF86662.1; -
DR InterPro: IPR003573; -
DR InterPro: IPR003574; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
SQ SEQUENCE 118 AA: 13834 MW: 62E97FD3BDEABEC CRC64;

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Query Match 23.6%; Score 253; DB 6; Length 118;
Best Local Similarity 44.9%; Pred. No. 2.3e-15;
Matches 53; Conservative 22; Mismatches 41; Indels 2; Gaps 1;

OY 97 EKDGCQSGFNEETCLVKITITGLFEVYLYQNRFSSSEQARA--VOMSTKYLIOPL 154
DB 1 EEDGCFPLAANHETCLRTSGLEFQWYLEHQAQFRSEENTRVSMLKNNRHILNTL 60
OY 155 OKKAKNLDAITTPDPTNNSLTCLKAQNOMQLDMTHILRSFKEFLQSSIRALROM 212
DB 61 RKVKVNFEGVTLKPAIVASLMENLQOKDMKTTIHIFILGLDIFLOFTLRSVRLM 118

Search completed: October 4, 2001, 19:12:00
Job time: 1186 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:09 ; Search time 54.44 Seconds
(without alignments)

234,968 Million cell updates/sec

Title: US-09-230-048-4

Perfect score: 1098
Sequence: 1 MKFLSANDHPVAFILGLMV.....FLKSLSEFLKVLKTLSTROT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 21: /SIDSI/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1098	100.0	211	14	AA1983385
2	1098	100.0	211	15	AA1990400
3	982	89.4	168	20	AA195013
4	944	86.0	211	11	AA1906847
5	422.5	38.5	212	22	AA195776
6	421.5	38.4	212	9	AA1981176
7	421.5	38.4	212	10	AA190121
8	420.5	38.3	212	8	AA190238
9	420.5	38.3	212	9	AA190269
10	420.5	38.3	212	10	AA190047
11	420.5	38.3	212	10	AA190047

12	420.5	38.3	212	10	AA190371	pBSF2-L8, AAP903
13	420.5	38.3	212	10	AA190436	Interferon-beta-2.
14	420.5	38.3	212	10	AA190469	Interleukin-6, Ho
15	420.5	38.3	212	11	AA1905415	Human B-cell diffe
16	420.5	38.3	212	14	AA1933384	Cytokine hIL-6, H
17	420.5	38.3	212	14	AA193430	IFN-beta-2a, Homo
18	420.5	38.3	212	14	AA194726	Human IL-6 (for mo
19	420.5	38.3	212	15	AA1949041	Human Interleukin-
20	420.5	38.3	212	15	AA1949249	Sequence of human
21	420.5	38.3	212	16	AA1972317	Interferon-beta2a,
22	420.5	38.3	212	21	AA1987816	Human IL-6 protein
23	419.5	38.2	212	13	AA1922125	Sequence of ovine
24	419.5	38.2	212	9	AA191156	Human B-cell diffe
25	416.5	37.9	212	18	AA195878	Human Interleukin-
26	416.5	37.9	212	18	AA193643	Human Interleukin-
27	416	37.9	211	13	AA1925279	Mutant human BCDP.
28	412	37.5	201	9	AA191162	Polypeptide with B
29	405.5	36.9	212	12	AA192521	B cell differentia
30	383	34.9	184	20	AA195012	Sheep Interleukin-
31	380	34.6	188	20	AA195011	Human Interleukin-
32	377.5	34.4	185	15	AA1945718	Full length Interl
33	376.5	34.3	185	10	AA194754	Sequence of varian
34	376	34.2	347	22	AA1972222	Fusion protein Npr
35	375.5	34.2	185	11	AA1905311	Segment of B-cell
36	375.5	34.2	185	15	AA1945720	Full length Interl
37	374.5	34.1	543	20	AA1903164	Chimeric sIL-6R/IL
38	373.5	34.0	183	15	AA1960125	Human Interleukin
39	373.5	34.0	184	9	AA191158	Polypeptide with B
40	373.5	34.0	184	11	AA1906352	Human B-cell stimu
41	373.5	34.0	184	11	AA1903914	Polypeptide with h
42	373.5	34.0	184	13	AA190783	Interleukin-6, A
43	373.5	34.0	184	15	AA1945990	Mutant Interleukin
44	373.5	34.0	184	15	AA1955256	Interleukin 6, Ho
45	373.5	34.0	184	16	AA1968623	B-cell differentia

ALIGNMENTS

RESULT 1	AA1933385	standard; peptide: 211 AA.
ID	AA1933385	
AC	AA1933385	
XX		
DE	15-JUL-1993 (first entry)	
XX		
DE	Cytokine mIL-6.	
XX		
KW	Cytokine family; leukemia inhibitory factor; LIF; interleukin-6; OSM;	
KW	granulocyte colony stimulating factor; G-CSF; oncostatin-M; hybrid;	
KW	IL-6; alpha-helix.	
XX		
OS	Mus musculus.	
XX		
PN	W09305169-A.	
XX		
PD	18-MAR-1993.	
XX		
PF	24-AUG-1992; 92MO-US07112.	
XX		
PR	30-AUG-1991; 91US-0753178.	
XX		
PA	(HUTC-) HUTCHINSON CANCER RES CENT FRED.	
XX		
PI	Rose TM, Todaro GJ;	
XX		
DR	WPI: 1993-100991/12.	
XX		
PT	Hybrid cytokine(s) contg. four helical regions - derived from	
PT	LIF, G-CSF, IL-6 or oncostatin-M, useful for treating Kaposi's	
PT	sarcoma, Rheumatoid arthritis, malignancies etc.	
XX		

PS Disclosure: Fig 1: 41pp; English.

XX The sequences in AAR33378-85 cytokines derived from the cytokine
CC family members leukemia inhibitory factor (LIF), granulocyte colony
CC stimulating factor (G-CSF), interleukin-6 (IL-6) and oncostatin-M
CC (OSM). These cytokines were used in the production of hybrid
CC cytokines which have unique physiological properties. The hybrid
CC cytokines comprise a first, second, third and fourth alpha-helical
CC region derived from the corresponding region of one of the cytokines
CC given each derived from a factor different from that which at least
CC one additional region of the cytokine is derived.

SO Sequence 211 AA;

Query Match 100.0%; Score 1098; DB 14; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.8e-100;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFLSRDHPVAFGLMLVTTTAFTPTSOYRRKDFEDTPNRPVYTSQVGLTRHYLM 60
DB 1 mkflsrdthpvaflgmlvtttatfptsqyrrgdfedtpnrvytsqvgllthvllw 60
QY 61 EIVEMRKEICNGNSDCMNDALAEENNLKLPETQRNDGCGYQGYNGEICLKISSGLLEY 120
DB 61 elvemrkeicngnsdcmmndalaennlklpelqrndgcyqgyngelclikissgllley 120
QY 121 HSYLEYMKNNLKDNNKDKARVLOQDTELLIHFNQEVKDLHKIVLPPTISNALITDKLES 180
DB 121 hsyleymknnlkdnkdkarvlgqrdecllhlfngevkdlhkivlptpsnalltdkles 180
QY 181 OKEMLRRTKTIQFIKLSLEFVKVTLRSTROT 211
DB 181 gkewlrrtktiqfllksleeflkvltlrstrqt 211

RESULT 2

AAAR49040
ID AAR49040 standard; protein; 211 AA.

XX AAR49040;

DT 06-SEP-1994 (first entry)

DE Murine Interleukin-6.

XX Interleukin 6; IL-6; thrombocytopoiesis; surgery; chemotherapy;
KW radiation therapy; bone marrow transplantation; cancer therapy;
KW neoplasia; anti-neoplastic activity.

XX Mus musculus.

XX WO9403492-A.

XX 17-FEB-1994.

XX 01-JUL-1993; 93WO-AU00324.

XX 06-AUG-1992; 92AU-0003983.

XX (LUDM-) LUDMIG INST CANCER RES.

XX (UYME) UNIV MELBOURNE.

XX Simpson RJ, Williams NT;

XX WPI; 1994-065607/08.

XX N-PSDB; AAQ55972.

PT New interleukin-6 variants - capable of stimulating
PT thrombocytopoiesis while exhibiting low hybridoma growth factor
PT activity

PS Disclosure: Page 31; 46pp; English.

XX This sequence is murine interleukin-6 (IL-6). IL-6 variants in
CC the form of non-full length molecules can stimulate, enhance or
CC facilitate thrombocytopoiesis without the side effects of other IL-6
CC activities. The IL-6 variants are useful for inducing
CC thrombocytopoiesis in thrombocytopenic patients following surgery,
CC chemotherapy, radiation therapy or bone marrow transplantation. The
CC IL-6 variants may also be useful in cancer therapy where the
CC fragments express anti-neoplastic activity.

SO Sequence 211 AA;

Query Match 100.0%; Score 1098; DB 15; Length 211;
Best Local Similarity 100.0%; Pred. No. 3.8e-100;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFLSRDHPVAFGLMLVTTTAFTPTSOYRRKDFEDTPNRPVYTSQVGLTRHYLM 60
DB 1 mkflsrdthpvaflgmlvtttatfptsqyrrgdfedtpnrvytsqvgllthvllw 60
QY 61 EIVEMRKEICNGNSDCMNDALAEENNLKLPETQRNDGCGYQGYNGEICLKISSGLLEY 120
DB 61 elvemrkeicngnsdcmmndalaennlklpelqrndgcyqgyngelclikissgllley 120
QY 121 HSYLEYMKNNLKDNNKDKARVLOQDTELLIHFNQEVKDLHKIVLPPTISNALITDKLES 180
DB 121 hsyleymknnlkdnkdkarvlgqrdecllhlfngevkdlhkivlptpsnalltdkles 180
QY 181 OKEMLRRTKTIQFIKLSLEFVKVTLRSTROT 211
DB 181 gkewlrrtktiqfllksleeflkvltlrstrqt 211

RESULT 3

AAW95013
ID AAW95013 standard; peptide; 188 AA.

XX AAW95013;

DT 21-MAY-1999 (first entry)

DE Mouse Interleukin-6 (IL-6) polypeptide.

XX Cytokine; Interleukin-B30; IL-B30; forensic science; cell proliferation;
KW inflammatory condition; drug screening; human; IL-6.

XX Mus sp.

XX WO9905280-A1.

XX 04-FEB-1999.

XX 24-JUL-1998; 98WO-US15423.

XX 25-JUL-1997; 97US-0900905.

XX (SCHE) SCHERING CORP.

XX Bazan JF;

XX WPI; 1999-142935/12.

XX Newly isolated or recombinant polynucleotide encoding mammalian
PT cytokine interleukin-B30 (IL-B30), including fragments - useful for
PT regulating activation, development, differentiation and function of
PT various cell types, and for diagnosing and treating conditions
PT associated with IL-B30

PS Disclosure: Page 11-12; 83pp; English.

XX This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
CC polypeptides. Host cells containing a vector comprising the IL-B30

CC nucleic acids are used for the recombinant production of the proteins.
 CC The polynucleotides are useful for diagnosis of IL-830 mediated
 CC conditions, and forensic science (e.g. to distinguish rodent from human,
 CC or as a marker to distinguish between different cells exhibiting
 CC differential expression or modification patterns). The IL-830 (including
 CC fragments), together with antibodies that bind to IL-830 are useful for
 CC teaching purposes. They are also used for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions. The polypeptide cytokine should mediate cytokine synthesis
 CC and proliferation in cells. IL-830 is useful for drug screening to
 CC identify compounds having binding affinity to IL-830. The present
 CC sequence represents a human IL-6.
 XX
 SO Sequence 188 AA:
 Query Match 89.48; Score 982; DB 20; Length 188;
 Best Local Similarity 100.0%; Pred. No. 8.3e-89;
 Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 24 APTSGVRGDFEDTTPNRPVYTTSGVGLTHVMEIYMRKELONGSDCKNNDAL 83
 DB 1 afptsgvrrdftedtpnrvpyttsqvgllthvmeivemrkelcngsdckmndal 60
 OY 84 AENNKLPEIQRNDGCVOTGYNOEICLKISSGLEHYHSTLEYKNNLKDKRKDKARYLQ 143
 DB 61 aennklpeiqrndgcvotgyngelcllkissgllchysyleyknmlkdkkdkarvlg 120
 OY 144 RDTETLHIFNQEKDHLKIVLPPTISNALLTDKLESQKELRRTIOFILKSLPEELKV 203
 DB 121 rdtetlhinqekdhlkivlpptisnalltdklesqkewlrtrtqifllksleeflkv 180
 OY 204 TLRSTROT 211
 DB 181 tlrstrqt 188
 RESULT 4
 ID AAR06847 standard; protein: 211 AA.
 AC AAR06847;
 XX 14-JAN-1991 (first entry)
 DE Rat interleukin-6 (IL-6).
 XX
 KW Immunostimulant; antitumour; antiinflammatory; cytokine.
 XX
 OS Rattus rattus.
 XX
 PN JP02195885-A.
 PD 02-AUG-1990.
 XX
 PF 25-JAN-1989; 89JP-0016806.
 XX
 PR 25-JAN-1989; 89JP-0016806.
 XX
 PA (SAKA) OTSUKA PHARM KK.
 XX
 DR WPI; 1990-278846/37.
 DR N-PSDB; AAO05965.
 XX
 PT Rat IL-6 gene - used in development of IL-6 for drugs e.g.
 PT Immunostimulant, antitumour drug, antiinflammatory drug etc.
 XX
 PS Claim 1; Page 553; 16pp; Japanese.
 CC IL-6 gene product may be useful in study and development of
 CC drugs eg. immunostimulants, antitumour drugs, cytokine production
 CC accelerators, antiinflammatory drugs and radiation damage inhibitors.
 XX

SO Sequence 211 AA:
 Query Match 86.08; Score 944; DB 11; Length 211;
 Best Local Similarity 85.38; Pred. No. 5.3e-85;
 Matches 180; Conservative 18; Mismatches 13; Indels 0; Gaps 0;
 OY 1 MKFISARDPHVAFILGMLVTTTAPPTSGVRGDFEDTTPNRPVYTTSGVGLTHVLM 60
 DB 1 mkfisdphvafilgmlvtatfpisqvrgrdftedtpnrvpyttsqvgllvylr 60
 OY 61 EIVEMRKELONGSDCKNNDALAEENKLPEIQRNDGCVOTGYNOEICLKISSGLEHY 120
 DB 61 eivemrkelcngsdckmndalaeennklpeiqrndgcvotgyngelcllkissgllf 120
 OY 121 HSTLEYKNNLKDKRKDKARVLPPTISNALLTDKLES 180
 DB 121 hstleyknnlkdkrkdkarvlpptisnalltdkles 180
 OY 181 QKEWLRTRTIOFILKSLPEELKVLTRSTROT 211
 DB 181 qkewlrtrtqifllksleeflkvltmrstrqt 211
 RESULT 5
 ID AAB49786 standard; protein: 212 AA.
 AC AAB49786;
 XX 23-APR-2001 (first entry)
 DE Human interferon beta 2a (IL-6) amino acid sequence.
 XX
 KW Human; keratinocyte derived interferon; KDI; viral infection; lymphoma;
 KW immune system related disorder; cancer; multiple sclerosis; AIDS;
 KW hepatitis; Cryptosporidium parvum infection; leukaemia; arthritis;
 KW diabetes; allergy; chronic myelogenous leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200107608-A1.
 PD 01-FEB-2001.
 XX
 PF 20-JAN-2000; 2000WO-US01239.
 XX
 PR 21-JUL-1999; 99US-0358587.
 XX
 PR 21-JUL-1999; 99WO-US16424.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Moore PA, LaPlaur DW;
 XX
 DR WPI; 2001-138557/14.
 XX
 PT Isolated keratinocyte derived interferon protein and polynucleotide
 PT used to prevent, treat or ameliorate an immune system-related disorder,
 PT viral infection, viral exposure and cancer -
 XX
 PS Disclosure; Fig 4; 303pp; English.
 CC This invention relates to human polynucleotide sequence AAF72333 which
 CC encodes keratinocyte derived interferon (KDI) protein AAB49774, which is
 CC a member of the interferon family. AAF72338 represents the codon
 CC optimised sequence of KDI. The human KDI gene is located on chromosome 9.
 CC The specification includes KDI related protein sequences
 CC AAB49775 - AAB49789. Also given in the specification are primer, probe
 CC and polynucleotide sequences represented by AAF72334-AAF72370 (excluding
 CC AAF72338) which are used in the isolation and characterisation of the KDI
 CC sequence of the invention. The KDI polypeptide is used to treat viral
 CC infections and the protein and polynucleotide may be used to prevent,
 CC treat or ameliorate a medical condition such as immune system-related


```

DE Interleukin-6.
XX
XX Interleukin-6; lysine-depleted variant;
KW site-directed mutagenesis; human.
XX
XX Homo sapiens.
OS
XX W08905824-A.
XX
XX
XX 29-JUN-1989.
XX
XX
XX 22-DEC-1988: 88WO-US04633.
XX
XX 23-DEC-1987: 87US-0137043.
XX
XX (GENE ) GENETICS INST INC.
XX
XX Shaw G;
XX
XX WPI: 1989-206594/28.
XX
XX N-PSDB; AAN90255.
XX
XX New lysine depleted variants of polypeptide
PT - opt. modified with hydrophilic residues,
PT biologically active but with altered solubility, stability etc.
XX
XX Disclosure; fig 3; 35pp; English.
XX
XX DNA of Interleukin-6 (see corresp. AAN90255). Used in the patent
CC to create lysine depleted variants by site-directed mutagenesis,
CC or syntheses.
XX
XX Sequence 212 AA;
SQ

Query Match 38.3%; Score 420.5; DB 10; Length 212;
Best Local Similarity 41.8%; Pred. No. 1.6e-33;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSARDHPVAF-LGLMLVTTTAPTSQVRKGFED-TTPNR-PVYTTSGVGLITH 57
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 mmsfetsaigpvalfsglllvlpafp-apvpsgedskvaaphrqlsaseridkqlry 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 VLMEIYEMRKELCNGSDCMNDALAEENNLKPEIQNDGCTGYNOEICLLKISSGL 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 lldglsalrkctcnksmcskskaelaennlnpkmaekdgcfsqfneetclvklitgl 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 LEYHSYLEYMKNNLKDNNKKDKARVLRDRETLIHIFNOEYKDLHKIVLPRTISNALLTDK 177
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 120 lsfeyyleylgnrf-esseeqaravqmsckvllqflqkxaknldaltcpdptnaallck 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY -178 LESQKEMLRKTQIQTILKSLSEPLKVTLRSTRQ 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 179 lqeqnqwlqdmthlllrfskellqslralrql 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
AAR05415
ID AAR05415 standard; protein; 212 AA.
XX
XX AAR05415;
XX
XX 27-JUL-1990 (first entry)
XX
XX Human B-cell differentiation factor gene product.
XX
XX BSF-2; dhfr; dihydrofolic acid reductase; differentiation.
XX
XX Homo sapiens.
OS
XX JP02009388-A.
XX
XX PN
XX
XX PD 12-JAN-1990.

```

```

XX
XX 08-JUL-1988: 88JP-0170142.
XX
XX 09-MAR-1988: 88JP-0055270.
XX
XX (AJIN ) AJINOMOTO KK.
XX
XX WPI: 1990-055348/08.
XX
XX N-PSDB; AAO01763.
XX
XX Physiologically active protein prepn.
XX
XX by transforming plasmid having gene coding physiologically
PT active protein and gene of dihydrofolic acid reductase to hamster
PT ovary etc.
XX
XX Example 3; Fig 6; 12pp; Japanese.
XX
XX Gene may be expressed by transforming a dhfr negative strain of CHO cells
CC with an active BSF-2 gene and dhfr carrying vector. BSF-2 gene product
CC is a B-cell differentiating factor.
XX
XX Sequence 212 AA;
SQ

Query Match 38.3%; Score 420.5; DB 11; Length 212;
Best Local Similarity 41.8%; Pred. No. 1.6e-33;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSARDHPVAF-LGLMLVTTTAPTSQVRKGFED-TTPNR-PVYTTSGVGLITH 57
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 mmsfetsaigpvalfsglllvlpafp-apvpsgedskvaaphrqlsaseridkqlry 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 58 VLMEIYEMRKELCNGSDCMNDALAEENNLKPEIQNDGCTGYNOEICLLKISSGL 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 60 lldglsalrkctcnksmcskskaelaennlnpkmaekdgcfsqfneetclvklitgl 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 118 LEYHSYLEYMKNNLKDNNKKDKARVLRDRETLIHIFNOEYKDLHKIVLPRTISNALLTDK 177
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 120 lsfeyyleylgnrf-esseeqaravqmsckvllqflqkxaknldaltcpdptnaallck 178
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 178 LESQKEMLRKTQIQTILKSLSEPLKVTLRSTRQ 210
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 179 lqeqnqwlqdmthlllrfskellqslralrql 211
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Search completed: October 4, 2001, 18:52:09
Job time: 1675 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:10:32 ; Search time 32.27 Seconds
(without alignments)
134.632 Million cell updates/sec

Title: US-09-230-048-4

Perfect score: 1098

Sequence: 1 MKFLSARDHPVAFILGLMLV.....FILKSLERFLKVLKSTROT 211

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: Issued_Patents_AA:*
- 2: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
- 6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1098	100.0	211	4	US-08-097-869-8
2	982	89.4	188	3	US-09-122-443-14
3	420.5	38.3	212	1	US-08-792-0198-9
4	420.5	38.3	212	3	US-08-988-819-9
5	420.5	38.3	212	4	US-09-016-534-9
6	420.5	38.3	212	4	US-08-097-869-7
7	420.5	38.3	212	4	US-08-795-4738-6
8	420.5	38.3	212	6	5510472-2
9	383	34.9	184	3	US-09-122-443-13
10	380	34.6	188	3	US-09-122-443-12
11	377.5	34.4	185	1	US-07-918-181A-4
12	377.5	34.4	185	1	US-08-231-575-4
13	375.5	34.2	185	5	PCT-US93-06928-4
14	375.5	34.2	185	1	US-07-918-181A-8
15	375.5	34.2	185	1	US-08-231-575-8
16	375.5	34.2	185	5	PCT-US93-06928-8
17	373.5	34.0	184	1	US-08-009-973-1
18	373.5	34.0	184	1	US-08-567-047-2
19	373.5	34.0	184	2	US-08-567-048-2
20	373.5	34.0	184	6	5186931-1
21	373.5	34.0	185	1	US-07-632-0708-1
22	373.5	34.0	185	1	US-07-918-181A-2
23	373.5	34.0	185	1	US-08-231-575-2
24	373.5	34.0	185	1	US-08-246-427A-5
25	373.5	34.0	185	2	US-08-716-317-7
26	373.5	34.0	185	2	US-08-766-620-5
27	373.5	34.0	185	5	PCT-US93-06928-2

28	373.5	34.0	185	6	5186931-2	Patent No. 5186931
29	373.5	34.0	186	1	US-07-632-0708-2	Sequence 2, Appl
30	373.5	34.0	186	1	US-07-745-382-20	Sequence 20, Appl
31	373.5	34.0	186	1	US-07-921-848-20	Sequence 20, Appl
32	373.5	34.0	186	1	US-08-165-301A-20	Sequence 20, Appl
33	373.5	34.0	186	1	US-08-469-318-163	Sequence 163, App
34	373.5	34.0	186	3	US-08-468-609A-163	Sequence 163, App
35	373.5	34.0	186	4	US-08-810-436-20	Sequence 20, Appl
36	373.5	34.0	186	5	PCT-US94-01185-163	Sequence 20, Appl
37	373.5	34.0	187	1	US-07-632-0708-3	Sequence 163, App
38	373.5	34.0	187	1	US-07-632-0708-3	Sequence 3, Appl
39	373.5	34.0	317	3	US-08-469-318-145	Sequence 145, App
40	373.5	34.0	317	3	US-08-468-609A-145	Sequence 145, App
41	373.5	34.0	317	5	PCT-US95-01185-145	Sequence 145, App
42	371.5	33.8	184	2	US-08-693-182-2	Sequence 2, Appl
43	371.5	33.8	184	2	US-09-008-482-2	Sequence 2, Appl
44	371.5	33.8	185	1	US-07-918-181A-6	Sequence 6, Appl
45	371.5	33.8	185	1	US-08-231-575-6	Sequence 6, Appl

ALIGNMENTS

```

RESULT 1
US-08-097-869-8
Sequence 8, Application US/08097869
Patent No. 6204364
GENERAL INFORMATION:
APPLICANT: Todaro, George J.
APPLICANT: Rose, Timothy M.
TITLE OF INVENTION: HYBRID CYTOKINES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,869
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/753,178
FILING DATE: 30-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24455-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 211 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-097-869-8

```

Query Match 100.0%; Score 1098; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 8.5e-103; Indels 0; Gaps 0;
Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKFLSARDHPVAFILGLMLVTTTAAFPVSQVRGDFTEDETPENRPVYTTSGVGLITHVLW 60

|||||
Db 1 MKFLSARDHPVAF-IGLMVTTTAPTSQVRKDEDTTPNRPVYTTSSQVGLTHVW 60
QY 61 EIVEMKRELKNGSDCMNDLAEENLKLPETIORNDGCYOTGYNOEICLKISSGLLEY 120
|||||
Db 61 EIVEMKRELKNGSDCMNDLAEENLKLPETIORNDGCYOTGYNOEICLKISSGLLEY 120
QY 121 HSYLEYMKNNLKDKKDKARVLORDTELTTHIFNOEVKDLHKIVLPPTPISNALLTDKLES 180
|||||
Db 121 HSYLEYMKNNLKDKKDKARVLORDTELTTHIFNOEVKDLHKIVLPPTPISNALLTDKLES 180
QY 181 OKEMLRKTIOFLKSLSEEFKVTLRSTROT 211
|||||
Db 181 OKEMLRKTIOFLKSLSEEFKVTLRSTROT 211
RESULT 2
US-09-122-443-14
Sequence 14, Application US/09122443
Patent No. 6060284
GENERAL INFORMATION:
APPLICANT: Bazan, J. Fernando
TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/122,443
FILING DATE: 24-JUL-1998
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/053,765
FILING DATE: 25-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0758K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
TELEFAX: (650)496-1200
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-122-443-14
Query Match 89.4%; Score 982; DB 3; Length 188;
Best Local Similarity 100.0%; Pred. No. 3,2e-91;
Matches 188; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|||||
Db 121 RDEETLTHIFNOEVKDLHKIVLPPTPISNALLTDKLESOKEMLRKTIOFLKSLSEEFKLV 180
QY 204 TLRSTROT 211
|||||
Db 181 TLRSTROT 188
RESULT 3
US-08-792-019B-9
Sequence 9, Application US/08792019B
Patent No. 5741772
GENERAL INFORMATION:
APPLICANT: CHANG, KING-SHI
TITLE OF INVENTION: THE NEUROTROPHIC FACTOR NNT-1
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN INC.
STREET: 1840 DEHAVILLAND DRIVE
CITY: THOUSAND OAKS
STATE: CA
COUNTRY: USA
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,019B
FILING DATE: 03-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: COOK, ROBERT R.
REGISTRATION NUMBER: 31,602
REFERENCE/DOCKET NUMBER: A-442
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..182
FEATURE:
NAME/KEY: Region
LOCATION: -30..0
US-08-792-019B-9
Query Match 38.3%; Score 420.5; DB 1; Length 212;
Best Local Similarity 41.8%; Pred. No. 9.4e-35;
Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

Query Match 38.3%; Score 420.5; DB 6; Length 212;
 Best Local Similarity 41.8%; Pred. No. 9.4e-35;
 Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

QY 1 MKFLSADPHVAF-LGLMVTYTAFTPTSOVRDFTED-TTPNR-PVYTSQVGLITH 57
 DB 1 MNSFSAFGVAFSLGLLVLPAAFP-APVPGEDSKDVAPRPHOPTTSSERIDKOIRY 59

QY 58 VLMEIVEMKELCGNSDCMNNDDALAEENNLKPEIORNDCGYGTGYNQICLKISSGL 117
 DB 60 ILDGISALRKETCKNSKNCESKALAEENNLKPEIAEKDCFGSGFNEETCLVKITIGL 119

QY 118 LEVHSLYEMKNNLKDKNKARVLRQRTETLHIFNOEVKDLHKVLPPISSNALITDK 177
 DB 120 LEFEVYLEYLRNRF-ESSEQARAVQSTKVLIQFLOKKAKNLDAITTPDPTNASSLITK 178

QY 178 LESQEWLRTTIQFIKLSLEEFKVLTRSTRQ 210
 DB 179 LQAGNOMLQDMWTHILRSFREFLOSSLRALRQ 211

RESULT 9
 US-09-122-443-13
 ; Sequence 13, Application US/09122443
 ; Patent No. 6060284
 ; GENERAL INFORMATION:
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/122.443
 ; FILING DATE: 24-JUL-1998
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/053.765
 ; FILING DATE: 25-JUL-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0758K1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)852-9196
 ; TELEFAX: (650)496-1200
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 184 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-122-443-13

Query Match 34.9%; Score 383; DB 3; Length 184;
 Best Local Similarity 40.1%; Pred. No. 4.6e-31;
 Matches 75; Conservative 44; Mismatches 62; Indels 6; Gaps 3;

QY 24 APTPSQVRGDTETPTNRPVYTT-SQVGLITHVLEIYEMKELCGNSDCMNNDDA 82
 DB 1 APTPGPLGEDEPKNDPTTSLTLTTPERTALIKHIVDKISAIKREICEKDECNSEKET 60

QY 83 LAENNLKPEIORNDCGYGTGYNQICLKISSGLLEYHSLYEMKNNLKDKNKARVL 142
 DB 61 LAEKMLPKMEKDGCGFSGFNQALICITKTAGLLEYQITLQDFLPESGN-QETVMEI 119

QY 143 QRDTELIHIFNOEVKDLHKVLPPISSNALITDKLESQEWLRTTKTIQFIKLSLEEFK 202
 DB 120 QSSIRTLQILKEKVIAGL---ITTPATHDMLEKMOSSNEVKNARVITILRSLENFIQ 175

QY 203 VTLRSTR 209
 DB 176 FSLRAIR 182

RESULT 10
 US-09-122-443-12
 ; Sequence 12, Application US/09122443
 ; Patent No. 6060284
 ; GENERAL INFORMATION:
 ; APPLICANT: Bazan, J. Fernando
 ; TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/122.443
 ; FILING DATE: 24-JUL-1998
 ; CLASSIFICATION: 436
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/053.765
 ; FILING DATE: 25-JUL-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Ching, Edwin P.
 ; REGISTRATION NUMBER: 34,090
 ; REFERENCE/DOCKET NUMBER: DX0758K1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (650)852-9196
 ; TELEFAX: (650)496-1200
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 188 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-122-443-12

Query Match 34.6%; Score 380; DB 3; Length 188;
 Best Local Similarity 40.7%; Pred. No. 9.4e-31;
 Matches 77; Conservative 49; Mismatches 59; Indels 4; Gaps 4;

QY 24 APTPSQVRGDTETPTNRPVYTT-SQVGLITHVLEIYEMKELCGNSDCMNNDD 81
 DB 1 APTPGPLGEDEPKNDVAPRPHOPTTSSERIDKOIRYILDGISALRKETCKNSKNCESKE 59

QY 82 ALAENNLKPEIORNDCGYGTGYNQICLKISSGLLEYHSLYEMKNNLKDKNKARV 141
 DB 60 ALAENNLKPEIAEKDCFGSGFNEETCLVKITIGLFEVYLEYLRNRF-ESSSEQARA 118

QY 142 LQRTETLIHIFNOEVKDLHKVLPPISSNALITDKLESQEWLRTTKTIQFIKLSLEEF 201
 DB 119 VOMSTKVLIQFLOKKAKNLDAITTPDPTNASSLITKLOAGNOMLQDMWTHILRSFREFL 178


```

1 APPLICATION NUMBER: US 07/918,181
2 FILING DATE: 23-JUL-1992
3 ATTORNEY/AGENT INFORMATION:
4 NAME: Felc, Irving N.
5 REGISTRATION NUMBER: 28,601
6 REFERENCE/DOCKET NUMBER: POW-2-T
7 TELECOMMUNICATION INFORMATION:
8 TELEPHONE: 212-645-1405
9 TELEFAX: 212-645-2054
10 INFORMATION FOR SEQ ID NO: 4:
11 SEQUENCE CHARACTERISTICS:
12 LENGTH: 185 amino acids
13 TYPE: amino acid
14 TOPOLOGY: linear
15 MOLECULE TYPE: protein
16 PCT-US93-06928-4
17
18 Query Match 34.4%; Score 377.5; DB 5; Length 185;
19 Best Local Similarity 41.1%, Pred.No.1.6e-30;
20 Matches 74; Conservative 48; Mismatches 55; Indels 3; Gaps 3;
21
22 QY 33 GDFETD-TTPNR-PVYTTSQVGILTHVLMEIVEVRKELTNGNSDDMMNDALAEENLKL 90
23 : ::::|::|::: |::|::: |::|::: |::|::: |::|::: |::|::: |
24 Db 6 GSDSDVAAPHROPILTSSBRIDKQIRIILDGISALRKETCKSNKCESSKEALAENNLT 65
25 : ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
26 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
27 QY 91 PEIQRNDGCYGTGYNOEICLKISSGLDEYHSLEYEMRNNLKNDRKARVLRQDTETLI 150
28 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
29 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
30 Db 66 PKMAEKDCFGSGFEETCLVIITIGLLEFYELYLNRF-ESESEQARAQMSTKVLI 124
31 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
32 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
33 QY 151 HIFNQVDLAKIVLPPTISNALLTDKLESQKEMWLRTKTIOFLKSLEBEFLKVTLRSTRO 210
34 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
35 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
36 Db 125 QLOKKARNLDIAITPPDPTTNASLLTKLAQNMQLDMTHILRSLEKFLQSSPLRALRO 184
37 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
38 : ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
39
40 RESULT 14
41 US-07-918-181A-8
42 Sequence 8, Application US/07918181A
43 Patent No. 5338833
44 GENERAL INFORMATION:
45 APPLICANT: Fowlkes, Dana M.
46 TITLE OF INVENTION: C-Terminal IL-6 Mutelins
47 NUMBER OF SEQUENCES: 35
48 CORRESPONDENCE ADDRESS:
49 ADDRESSEE: Imclone Systems Incorporated
50 STREET: 180 Varlick Street
51 CITY: New York
52 STATE: New York
53 COUNTRY: United States
54 ZIP: 10014
55 COMPUTER READABLE FORM:
56 MEDIUM TYPE: Floppy disk
57 COMPUTER: IBM PC compatible
58 OPERATING SYSTEM: PC-DOS/MS-DOS
59 SOFTWARE: Patentin Release #1.0, Version #1.25
60 CURRENT APPLICATION DATA:
61 APPLICATION NUMBER: US/07/918,181A
62 FILING DATE: 23-JUL-1992
63 CLASSIFICATION: 435
64 ATTORNEY/AGENT INFORMATION:
65 NAME: Sheets, Eric J.
66 REGISTRATION NUMBER: 30,326
67 REFERENCE/DOCKET NUMBER: POW-2
68 TELECOMMUNICATION INFORMATION:
69 TELEPHONE: 212-645-1405
70 TELEFAX: 212-645-2054
71 INFORMATION FOR SEQ ID NO: 8:
72 SEQUENCE CHARACTERISTICS:
73 LENGTH: 185 amino acids
74 TYPE: amino acid
75 TOPOLOGY: linear
76 MOLECULE TYPE: protein
77 US-07-918-181A-8

```

Query Match	34.2%	Score 375.5	DB 1	Length 185
Best Local Similarity	40.6%	Pred. No. 2.6e-30		
Matches 73	Conservative 49	Mismatches 55	Indels 3	Gaps 3
QY	33 GDFTE-D-TTPNR-PVYTTSSQVGLITTHVLMETVEIKKELCNSDSCMNNDALAEINNL	90		
DB	6 GEDSDVAPAHPIROPLTSSERIDKQIRYIIDGISALRKETCNKSNCESSKEALAEINNL	65		
QY	91 PEIQNDGCGYQGVNOECLIKISSGLEHYHLYEYMKNNLNKDKKARVQRTETELI	150		
DB	66 PMAEKDCQFSGFNEEFCVLKVIITGLLEFYLEYLELQNR-ESSEEDQARAQMSKTVLI	124		
QY	151 HIFNEVDMLIKIVLPFTFISNALLTDKLESQKEMLRPTIOTIFLSLEFLVTRSTPO	210		
DB	125 QELQKANNLAIITTPDDPTTNMSLLTKLQAOQWQMDMTTHILNLSKEFMQSSILRALQ	184		
RESULT 15				
US-08-231-575-8				
Sequence 8, Application US/08231575				
Patent No. 5565336				
GENERAL INFORMATION:				
APPLICANT: Fowles, Dana M.				
TITLE OF INVENTION: C-Terminal IL-6 Mutelins				
NUMBER OF SEQUENCES: 35				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Imclone Systems Incorporated				
STREET: 180 Varick Street				
CITY: New York				
STATE: New York				
COUNTRY: United States				
ZIP: 10014				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Floppy disk				
COMPUTER: IBM PC compatible				
OPERATING SYSTEM: PC-DOS/MS-DOS				
SOFTWARE: PatentIn Release #1.0, Version #1.25				
CURRENT APPLICATION DATA:				
APPLICATION NUMBER: US/08/231,575				
FILING DATE: 22-APR-1994				
CLASSIFICATION: 435				
PRIOR APPLICATION DATA:				
APPLICATION NUMBER: US 07/918,181				
FILING DATE: 23-JUL-1992				
ATTORNEY/AGENT INFORMATION:				
NAME: Sheets, Eric J.				
REGISTRATION NUMBER: 30,326				
REFERENCE/DOCKET NUMBER: POW-2				
TELECOMMUNICATION INFORMATION:				
TELEPHONE: 212-645-1405				
TELEFAX: 212-645-2054				
INFORMATION FOR SEQ ID NO: 8:				
SEQUENCE CHARACTERISTICS:				
LENGTH: 185 amino acids				
TYPE: amino acid				
TOPOLOGY: linear				
MOLECULE TYPE: protein				
US-08-231-575-8				
Query Match	34.2%	Score 375.5	DB 1	Length 185
Best Local Similarity	40.6%	Pred. No. 2.6e-30		
Matches 73	Conservative 49	Mismatches 55	Indels 3	Gaps 3
QY	33 GDFTE-D-TTPNR-PVYTTSSQVGLITTHVLMETVEIKKELCNSDSCMNNDALAEINNL	90		
DB	6 GEDSDVAPAHPIROPLTSSERIDKQIRYIIDGISALRKETCNKSNCESSKEALAEINNL	65		
QY	91 PEIQNDGCGYQGVNOECLIKISSGLEHYHLYEYMKNNLNKDKKARVQRTETELI	150		
DB	66 PMAEKDCQFSGFNEEFCVLKVIITGLLEFYLEYLELQNR-ESSEEDQARAQMSKTVLI	124		
QY	151 HIFNEVDMLIKIVLPFTFISNALLTDKLESQKEMLRPTIOTIFLSLEFLVTRSTPO	210		
DB	125 QELQKANNLAIITTPDDPTTNMSLLTKLQAOQWQMDMTTHILNLSKEFMQSSILRALQ	184		

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:09:55 ; Search time 44.98 Seconds
(without alignments)
357.333 Million cell updates/sec

Title: US-09-230-048-4

Perfect score: 1098

Sequence: 1 MKFLSARDHPVAFELGLMV.....FLKSLERFLKVLINSTRQT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_68:***
2: PIR1:***
3: PIR2:***
4: PIR3:***
5: PIR4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1098	100.0	211	1 ICMS6	interleukin-6 prec
2	944	86.0	211	2 A34247	interleukin-6 prec
3	432.5	39.4	212	2 I46590	interleukin 6 - pl
4	428.5	39.0	212	2 I46621	interleukin 6 - pl
5	422.5	38.5	208	1 A56610	interleukin-6 prec
6	420.5	38.3	208	1 S29549	interleukin-6 - sh
7	420.5	38.3	212	1 IVH082	interleukin-6 prec
8	414.5	37.8	208	2 T09216	interleukin-6 prec
9	337	30.7	207	2 I46084	interleukin 6 - ca
10	96	8.7	819	2 T19351	hypothetical prote
11	95	8.7	201	2 A42247	myelomonocytic gro
12	93.5	8.5	534	2 S57974	hypothetical prote
13	92.5	8.4	261	2 B64746	yeast protein - Esc
14	91.5	8.3	2663	1 S28261	centromere protein
15	90.5	8.2	1137	2 T28317	ORF MSV156 hypote
16	90.5	8.2	2042	2 T18399	variant-specific s
17	86.5	7.9	480	2 H86411	protein FIK23.12 l
18	86.5	7.8	743	2 D84545	probable salt-indu
19	85.5	7.9	1516	2 E71619	RAM2 endonuclease
20	85	7.7	2401	2 T28676	thymocyte protein -
21	84.5	7.7	1156	2 B70356	chromosome assembl
22	84.5	7.7	1228	2 A57384	multimerin, endoth
23	84	7.7	636	2 H70184	methy1-accepting c
24	84	7.7	785	2 T23452	hypothetical prote
25	84	7.7	785	2 T23456	hypothetical prote
26	84	7.7	1166	2 T27075	hypothetical prote
27	84	7.7	1354	2 S74244	serine/threonine-s
28	83.5	7.6	162	2 H71486	hypothetical prote
29	83.5	7.6	1354	2 S69211	serine/threonine-s

30	83.5	7.6	1417	2 T18418	hypothetical prote
31	83.5	7.6	1532	2 T18438	hypothetical prote
32	83	7.6	1170	2 A56157	chromosome segrega
33	83	7.6	2304	2 T07920	probable acetyl-Co
34	83	7.6	8243	2 T31307	type I fatty acid
35	82.5	7.5	750	2 T38435	coiled coil protei
36	82.5	7.5	911	2 JC7186	alpha-actinin-4 -
37	82.5	7.5	1076	2 C70007	hypothetical prote
38	82	7.5	720	2 JC6562	heat shock prote
39	82	7.5	758	2 S60586	glucocorticoid rec
40	82	7.5	1365	2 T18419	hypothetical prote
41	81.5	7.4	326	2 S49337	hypothetical prote
42	81.5	7.4	594	2 A82913	hypothetical prote
43	81.5	7.4	635	2 G86589	hypothetical prote
44	81.5	7.4	635	2 G72035	regulatory protein
45	81	7.4	176	2 A56652	interleukin-7 prec

ALIGNMENTS

RESULT 1

ICMS6
Interleukin-6 precursor - mouse
N:Alternate names: B-cell hybridoma growth factor; B-cell stimulating factor 2; hepat acyloma growth factor
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence, revision 30-Jun-1990 #text, change 22-Jun-1999
C:Accession: A30531, A27610, A30571, S01323, S12103, E34047, A26662, A40486, A60799;
R:Janabe, O.; Akira, S.; Kam19A, T.; Wong, G.G.; Hlranu, T.; Kishimoto, T.
J. Immunol. 141, 3875-3881, 1988
A>Title: Genomic structure of the murine IL-6 gene. High degree conservation of poten
A:Reference number: A30531; MUID:89035525
A:Accession: A30531

A:Molecule type: DNA
A:Residues: 1-211 <TAN>
A:Cross-references: GB:M20572; NID:g198369; PIDN:AAA3302.1; PID:g387386
R:Van Snick, J.; Cayphas, S.; Szikora, J.P.; Renaud, J.C.; Van Roost, E.; Boon, T.; Eur. J. Immunol. 18, 193-197, 1988
A>Title: CDNA cloning of murine interleukin-Hp1: homology with human interleukin 6.
A:Reference number: A27610; MUID:88166883
A:Accession: A27610

A:Molecule type: mRNA
A:Residues: 1-211 <VNA>
A:Cross-references: GB:X06203; NID:g52701; PIDN:CA29560.1; PID:g52702
R:Mock, B.A.; Nordan, R.P.; Justice, M.J.; Kozak, C.; Jenkins, N.A.; Copeland, N.G.; J. Immunol. 142, 1372-1376, 1989
A>Title: The murine IL-6 gene maps to the proximal region of chromosome 5.
A:Reference number: A30571; MUID:89124383
A:Accession: A30571

A:Molecule type: mRNA
A:Residues: 5-211 <MOC>
A:Cross-references: GB:M24223; NID:g341131; PIDN:AAA68614.1; PID:g870699
R:Simpson, R.J.; Moritz, R.L.; Rubira, M.R.; Van Snick, J. Eur. J. Biochem. 176, 187-197, 1988
A>Title: Murine hybridoma/plasmacytoma growth factor. Complete amino-acid sequence an
A:Reference number: S01323; MUID:88329059
A:Accession: S01323

A:Molecule type: protein
A:Residues: 25-166, X, 168-211 <STM>
A>Note: the sequence from Fig. 11 is inconsistent with that from Fig. 10 in having 10
R:Greenelt, H.E.; Fuentes, N.L.; Fuller, G.M. Nucleic Acids Res. 18, 6455, 1990
A>Title: Cloning and sequence analysis of the cDNA for murine interleukin-6.
A:Reference number: S12103; MUID:91057159
A:Accession: S12103

A:Molecule type: mRNA
A:Residues: 1-211 <GRE>
A:Cross-references: EMBL:X54542; NID:g52727; PIDN:CA38411.1; PID:g52728
R:Jahnen, W.; Ward, L.D.; Reid, G.E.; Moritz, R.L.; Simpson, R.J. Biochem. Biophys. Res. Commun. 166, 139-145, 1990
A>Title: Internal amino acid sequencing of proteins by in situ cyanogen bromide cleav
A:Reference number: A90157; MUID:90147691

A:Accession: E34047
 A:Molecule type: protein
 A:Residues: 66-69,'X','71-75;78-94;128-148 <UA5>
 R:Van Snick, J.; Cayphas, S.; Vink, A.; Uytendhoe, C.; Coullie, P.G.; Rubira, M.R.; Simg
 Proc. Natl. Acad. Sci. U.S.A. 83, 9679-9683, 1986
 A:Title: Purification and NH₂-terminal amino acid sequence of a T-cell-derived lymphokine
 A:Reference number: A26662; MUID:87092311
 A:Accession: A26662
 A:Molecule type: protein
 A:Residues: 25-39,'X','41-42,'X','44-45 <VSN>
 R:Chiu, C.P.; Moulds, C.; Coffman, R.L.; Rennick, D.; Lee, F.
 Proc. Natl. Acad. Sci. U.S.A. 85, 7099-7103, 1988
 A:Title: Multiple biological activities are expressed by a mouse interleukin 6 cDNA clone
 A:Reference number: A40486; MUID:89017145
 A:Accession: A40486
 A:Molecule type: mRNA
 A:Residues: 1-211 <CHI>
 A:Cross-references: GB:J03783; NID:9198367; PIDN:AA39301.1; PID:9309410
 R:Shabo, Y.; Ischem, J.; Rudinshtein, M.; Revel, M.; Clark, S.C.; Moll, S.F.; Kamen, R.; S
 Blood 72, 2070-2073, 1988
 A:Title: The myeloid blood cell differentiation-inducing protein MGI-2A is interleukin-6
 A:Reference number: A60799; MUID:89062753
 A:Accession: A60799
 A:Molecule type: protein
 A:Residues: 77-98 <SHN>
 R:Blankenstein, T.; Qin, Z.; Li, W.; Diamantstein, T.
 J. Exp. Med. 171, 965-970, 1990
 A:Title: DNA rearrangement and constitutive expression of the interleukin 6 gene in a mc
 A:Reference number: S10241; MUID:90171860
 A:Accession: S10241
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-6 <BLA>
 A:Cross-references: EMBL:X51457; NID:949738; PIDN:CAA35824.1; PID:9581860
 R:Zheng, J.C.; Reid, G.E.; Moritz, R.L.; Ward, L.D.; Simpson, R.J.
 Eur. J. Biochem. 217, 53-59, 1993
 A:Title: Specific covalent modification of the tyrophophan residues in murine interleukin
 A:Reference number: S38254; MUID:94039075
 A:Accession: S38254
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 38-60;75,'X','77-79;176-203 <ZHA>
 C:Genetics:
 A:Gene: IL-6
 A:Map position: 5
 A:Introns: 7/1; 68/3; 106/3; 156/3
 C:Supportfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; growth factor; immunoregulation; lymphokine;
 F:1-24/Domains: signal sequence #status predicted <SIG>
 F:25-211/Product: Interleukin-6 #status experimental <MAT>

Query Match 100.0%; Score 1098; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 5.2e-82;
 Matches 211; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTVLM 60
 DB 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTVLM 60
 QY 61 EIVEKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSGLEY 120
 DB 61 EIVEKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSGLEY 120
 QY 121 HSYLEYMKNLNDKDKARVLRQRTETLIHFNQEVKDLKIVLPTPISNALLTDKLES 180
 DB 121 HSYLEYMKNLNDKDKARVLRQRTETLIHFNQEVKDLKIVLPTPISNALLTDKLES 180
 QY 181 OKEWLRTKTIOFTILKSLEEFKLVTRSTROT 211
 DB 181 OKEWLRTKTIOFTILKSLEEFKLVTRSTROT 211

RESULT 2
 A34247
 Interleukin-6 precursor - rat
 N:Alternate names: IL-6
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 16-Jul-1999
 C:Accession: A34247
 R:Northmann, W.; Brackak, T.A.; Hattori, M.; Lee, F.; Fey, G.H.
 J. Biol. Chem. 264, 16072-16082, 1989
 A:Title: Structure of the rat interleukin 6 gene and its expression in macrophage-der
 A:Reference number: A34247; MUID:89380206
 A:Accession: A34247
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-211 <NOR>
 A:Cross-references: GB:M6744; NID:9204915; PIDN:AA7659.1; PID:9204916
 C:Superfamily: Interleukin-6
 C:Keywords: cytokine; growth factor; immunoregulation; lymphokine; macrophage

Query Match 86.0%; Score 944; DB 2; Length 211;
 Best Local Similarity 85.3%; Pred. No. 1.6e-69;
 Matches 180; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTVLM 60
 DB 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTVLM 60
 QY 61 EIVEKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSGLEY 120
 DB 61 EIVEKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSGLEY 120
 QY 121 HSYLEYMKNLNDKDKARVLRQRTETLIHFNQEVKDLKIVLPTPISNALLTDKLES 180
 DB 121 HSYLEYMKNLNDKDKARVLRQRTETLIHFNQEVKDLKIVLPTPISNALLTDKLES 180
 QY 181 OKEWLRTKTIOFTILKSLEEFKLVTRSTROT 211
 DB 181 OKEWLRTKTIOFTILKSLEEFKLVTRSTROT 211

RESULT 3
 Interleukin 6 - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 16-Jul-1999
 C:Accession: I46590
 R:Mathialagan, N.; Bixby, J.; Roberts, M.R.
 Mol. Reprod. Dev. 32, 324-330, 1992
 A:Title: Expression of Interleukin-6 in porcine, ovine, and bovine preimplantation co
 A:Reference number: I46590; MUID:92360284
 A:Accession: I46590
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAT>
 A:Cross-references: GB:M60258; NID:9164514; PIDN:AA27127.1; PID:9164515
 C:Genetics:
 A:Gene: IL-6
 C:Superfamily: Interleukin-6

Query Match 39.4%; Score 432.5; DB 2; Length 212;
 Best Local Similarity 42.7%; Pred. No. 4.9e-28;
 Matches 90; Conservative 42; Mismatches 76; Indels 3; Gaps 3;

QY 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTV 58
 DB 1 MKFLSARDFHPAFLGMLVTTTAPTSQVRGDEFTEDTPNRPVYTTSQVGLITHTV 58
 QY 59 LMEIEMKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSG 118
 DB 59 LMEIEMKREKELCNGSDCMNDDALAENNLKLPETIORNDGCGYGYNOEICLLKISSG 118

A>Note: the authors translated the codon CAG for residue 130 as Glu
 R.Zilberstein, A.; Ruggieri, R.; Korn, J.H.; Revel, M.
 EMBO J. 5, 2529-2537, 1986
 A>Title: Structure and expression of cDNA and genes for human Interferon-beta-2, a distinct
 A:Reference number: A91051; MUID:87053818
 A:Accession: A25692
 A:Molecule type: mRNA
 A:Residues: 1-212 <212>
 A:Cross-references: GB:X04430; NID:932673; PIDN:CA28026.1; PID:932674
 R.Hirano, T.; Yasukawa, K.; Harada, H.; Taga, T.; Matsuda, T.; Kishimura
 I. T.; Kishimoto, T.
 Nature 334, 73-76, 1986
 A>Title: Complementary DNA for a novel human Interleukin (BSF-2) that induces B lymphocyte
 A:Reference number: A93387; MUID:87065033
 A:Accession: A26966
 A:Molecule type: mRNA
 A:Residues: 1-212 <HIR>
 A:Cross-references: GB:X04602; NID:933849; PIDN:CA28268.1; PID:933850
 R.Tonouchi, N.; Miwa, K.; Kurasayama, H.; Matsui, H.
 Biochem. Biophys. Res. Commun. 163, 1056-1062, 1989
 A>Title: Deletion of 3' untranslated region of human BSF-2 mRNA causes stabilization of
 A:Reference number: A33515; MUID:89391958
 A:Accession: A33515
 A:Molecule type: mRNA
 A:Residues: 1-212 <TON>
 A:Cross-references: GB:M29150; NID:9186349; PIDN:AA59154.1; PID:9307063
 R.Hageman, G.; Content, J.; Volckaert, G.; Derynck, R.; Tavernier, J.; Fiers, W.
 Eur. J. Biochem. 159, 625-633, 1986
 A>Title: Structural analysis of the sequence coding for an inducible 26-kDa protein in h
 A:Reference number: A25801; MUID:87004683
 A:Accession: A25801
 A:Molecule type: DNA; mRNA
 A:Residues: 1-212 <HAE>
 A:Cross-references: GB:X04403
 A:Experimental source: fibroblast
 R.May, L.T.; Helfgott, D.C.; Sehgal, P.B.
 Proc. Natl. Acad. Sci. U.S.A. 83, 8957-8961, 1986
 A>Title: Anti-beta-interferon antibodies inhibit the increased expression of HLA-B7 mRNA
 A:Reference number: A25921; MUID:87067433
 A:Accession: A25921
 A:Molecule type: mRNA
 A:Residues: 1-212 <MAV>
 A:Cross-references: GB:M4584; NID:9184628; PIDN:AA52278.1; PID:9306910
 R.Wong, G.G.; Witek-Glannott, J.; Hewick, R.M.; Clark, S.C.; Ogawa, M.
 Beirntg Inst. Molec. Biol. 83, 40-47, 1988
 A>Title: Interleukin 6: identification as a hematopoietic colony-stimulating factor.
 A:Reference number: I52193; MUID:89193317
 A:Accession: I52193
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <MON>
 A:Cross-references: GB:M54894; NID:9186351; PIDN:AA641704.1; PID:9186352
 R.Braekhoff, J.P.; de Groot, E.R.; Evers, R.F.; Pannekoek, H.; Aarden, L.A.
 J. Immunol. 139, 4116-4121, 1987
 A>Title: Molecular cloning and expression of hybridoma growth factor in Escherichia coli
 A:Reference number: I56003; MUID:88088768
 A:Accession: I56003
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-212 <BRA>
 A:Cross-references: NID:9184631; PIDN:AA522729.1; PID:9306911
 R.Van Damme, J.; Van Beeumen, J.; Decock, B.; Van Snick, J.; De Ley, M.; Billiau, A.
 J. Immunol. 140, 1534-1541, 1988
 A>Title: Separation and comparison of two monokines with lymphocyte-activating factor ac
 A:Reference number: A92816; MUID:88154445
 A:Accession: A27601
 A:Molecule type: Protein
 A:Residues: 28-51, 'X', 53-57, 'X', 59, 'X', 61 <VANI>
 A:Accession: B27601
 A:Molecule type: Protein
 A:Residues: 30-56, 'XX', 59-61, 'X', 63 <VA2>
 R.Yamamoto, R.; Lin, L.S.; Lowe, R.; Warren, M.K.; White, T.J.
 J. Immunol. 144, 1808-1816, 1990

A>Title: The human lung fibroblast cell line, MRC-5, produces multiple factors involv
 A:Reference number: A60400; MUID:90171574
 A:Accession: A60400
 A:Molecule type: Protein
 A:Residues: 30-43 <YAM>
 R.Hirano, T.; Taga, T.; Yasukawa, K.; Nakajima, K.; Nakano, N.; Takatsuki, F.; Shimizu
 Proc. Natl. Acad. Sci. U.S.A. 84, 228-231, 1987
 A>Title: Human beta-cell differentiation factor defined by an anti-peptide antibody a
 A:Reference number: A29085; MUID:87092370
 A:Accession: A29085
 A:Molecule type: Protein
 A:Residues: 29-42 <HIR>
 R.Noda, M.; Takeda, K.; Sugimoto, H.; Hosoi, T.; Takeuchi, K.; Hara, T.; Ishikawa, H.;
 Anticancer Res. 11, 961-968, 1991
 A>Title: Purification and characterization of human fibroblast derived differentiat
 A:Reference number: A61159; MUID:91290785
 A:Accession: A61159
 A:Molecule type: Protein
 A:Residues: 30-42 <NOD>
 A:Experimental source: fibroblast
 R.Ming, J.E.; Gernetti, C.; Steinman, R.M.; Graneli-Piperno, A.
 J. Mol. Cell. Immunol. 4, 203-212, 1989
 A>Title: Interleukin 6 is the principal cytolytic T lymphocyte differentiation factor
 A:Reference number: A61462; MUID:90121567
 A:Accession: A61462
 A:Molecule type: Protein
 A:Residues: 28-48 <MIN>
 A:Experimental source: leukocyte-conditioned medium
 R.May, L.T.; Shaw, J.E.; Khanna, A.K.; Zdravkovic, J.B.; Sehgal, P.B.
 Cytokine 3, 204-211, 1991
 A>Title: Marked cell-type-specific differences in glycosylation of human Interleukin-
 A:Reference number: A48419; MUID:91353644
 A:Accession: A48419
 A:Molecule type: Protein
 A:Residues: 30-37, 'X', 39-40 <MAY2>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone
 A>Note: this 28-30k form contained both N-linked and O-linked carbohydrate: a 25k for
 A:Accession: C48419
 A:Molecule type: Protein
 A:Residues: 28-40 <MAY3>
 A:Experimental source: FS-4 fibroblasts
 A>Note: sequence extracted from NCBI backbone (NCBI:63787)
 A>Note: this 23-25k form contained O-linked but not N-linked carbohydrate
 R.Orita, T.; Oheida, M.; Hasegawa, M.; Kuboniva, H.; Esaki, K.; Ochi, N.
 J. Biochem. 115, 345-350, 1994
 A>Title: Polypeptide and carbohydrate structure of recombinant human Interleukin-6 pr
 A:Reference number: JX0305; MUID:94266765
 A:Accession: JX0305
 A:Contents: annotation; modified sites in recombinant protein from CHO cells
 R.Clogston, C.L.; Boone, T.C.; Granda, C.; Mendiaz, E.A.; Lu, H.S.
 Arch. Biochem. Biophys. 272, 144-151, 1989
 A>Title: Disulfide structures of human Interleukin-6 are similar to those of human gr
 A:Reference number: S04981; MUID:89286115
 A:Contents: annotation; disulfide bonds in recombinant protein
 R.Rock, F.L.; Li, X.; Chong, P.; Ide, N.; Klein, M.
 Biochemistry 33, 5146-5154, 1994
 A>Title: Roles of disulfide bonds in recombinant human Interleukin 6 conformation.
 A:Reference number: A54253; MUID:94227044
 A:Contents: annotation; lability and functional significance of each disulfide bond
 C:Comment: Produced by both lymphoid and nonlymphoid tissue in response to growth fac
 C:Comment: This protein plays a regulatory role in various host defense mechanisms an
 C:Genetics:
 A:Gene: GDB: IL6
 A:Cross-references: GDB:120748; OMIM:147620
 A:Map position: 7p21-7p21
 A:Introns: 7/1; 70/3; 108/3; 157/3
 C:Superfamily: Interleukin-6
 C:Keywords: Castleman's disease; cytokine; extracellular protein; glycoprotein; growt
 F:1-27/DNA: signal sequence #status predicted <SIG>
 F:28-212/Product: Interleukin-6, long form #status experimental <MAT>
 F:30-212/Product: Interleukin-6, short form #status experimental <MAT>
 F:72-78,101-111/Disulfide bonds: #status experimental


```

RESULT 11
AA2247
myelomonocytic growth factor precursor - chicken
N:Alternate names: colony-stimulating factor CMGF
C:Species: Gallus gallus (chicken)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:Accession: AA2247; S03633
R:Sternick, E.; Blattner, C.; Graf, T.; Leutz, A.
Mol. Cell. Biol. 12, 1728-1735, 1992
A>Title: Structure of the chicken myelomonocytic growth factor gene and specific activat
A:Reference number: AA2247; MUID:92195319
A:Accession: AA2247
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-201 <STE>
A>Note: sequence extracted from NCHI backbone (NCBI:89832, NCBI:89836)
R:Leutz, A.; Damm, K.; Sternick, E.; Kowenz, E.; Ness, S.; Frank, R.; Gausepohl, H.; Pan
EMBO J. 8, 175-181, 1989
A>Title: Molecular cloning of the chicken myelomonocytic growth factor (CMGF) reveals re
A:Reference number: S03633; MUID:89231616
A:Accession: S03633
A:Molecule type: mRNA
A:Residues: 1-201 <LEU>
A:Cross-references: EMBL:X14477; NID:963596; PIDN:CAA32639.1; PID:963597
C:Superfamily: Interleukin-6
C:Keywords: glycoprotein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-201/Product: myelomonocytic growth factor #status predicted <MAT>
F:123-137/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match      8.7%  Score 95; DB 2; Length 201;
Best Local Similarity 21.7%  Pred. No. 1.1;
Matches 34; Conservative 29; Mismatches 74; Indels 20; Gaps 5;

QY 61 EIVEKRELCNGSDCMNDALAEENMLKLPETQRNDGCTGYNOETCLIKISSLEY 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 52 DVVALQRAVCDPFOCTEEELQVOPDPIHLYAPL-DOCHKRGFAEVCFTQIRGLAHY 110
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 HSYLEVMKNNLKDKKKARVLRQRTETLIHIFNOEVKD--LHKIVLP-----PISNA 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 111 HDSLGAVL-RILPNTTLYETLQLDANLSSNQQOMEDGLDTYVLPFGQSPPTFSG 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 173 LITDKLESQKEMLRKTITQIFILKSLEEFKYLKSTR 209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 170 PFOQVGC-----FFILANFQRIETAYRALR 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
S57974
hypothetical protein YDR147w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YD8358.04
C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 29-Oct-1999
C:Accession: S57974
R:Murphy, L.; Richards, C.; Harlis, D.
submitted to the EMBL Data Library, July 1995
A:Reference number: S57971
A:Accession: S57974
A:Molecule type: DNA
A:Residues: 1-534 <MUR>
A:Cross-references: EMBL:Z50046; NID:9899393; PID:9899397; GSPDB:GN00004; MIPS:YDR147w
A:Experimental source: strain AB972
C:Genetics:
A:Gene: MIPS:YDR147w
A:Map position: 4R

Query Match      8.5%  Score 93.5; DB 2; Length 534;
Best Local Similarity 21.5%  Pred. No. 4.7;
Matches 52; Conservative 47; Mismatches 68; Indels 75; Gaps 13;

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QY 5 SARDFHPVAFGLMLVTTTAPFTSOVRGDF-----TEDTPNRPVYTT 48
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 81 TANDFLKLAVYNAKL--DPSLP-SQYFKODIINVLOSLEIPGMSVPGSSESLNNKLLTL 137
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 49 SOVGGLITVLMEL-----VEMKRELCNGSDCMNDALAEENMLKLPETQRNDGCTQ 101
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 138 TQIKGALTNVYIKIHYPNLPILMR--IFGDS----IDSVIDREYELKVIARL-SFYD 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 102 TGYNOETCLIKISSGLLEHYSLEYEMKNNLKDKKARVLRQRTETLIHIFNOEVKDL 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 LGPKLE-----GFENGRFEKYLEGSRSTQAD---FIDRDSIKI---AKLKEIH 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 162 KIVLPPTISNALLPDK-----LESQKEW-----LRTKTITQIFILKSLE 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 235 CTIV---PLTRHKEITDQPSCTFTFDQMIKLIDSHKEWVSNVNNISEILROSSWNFFLKSPK 291
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 199 EF 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 292 NY 293
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 13
B64746
yafT protein - Escherichia coli
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 04-Mar-2000
C:Accession: B64746
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: B64746
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-261 <BLAT>
A:Cross-references: GB:AE000130; GB:U00096; NID:917866402; PIDN:AAC73321.1; PID:9178664
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: yafT
C:Superfamily: Escherichia coli yafT protein

Query Match      8.4%  Score 92.5; DB 2; Length 261;
Best Local Similarity 26.3%  Pred. No. 2.4;
Matches 50; Conservative 26; Mismatches 81; Indels 33; Gaps 10;

```

```

QY 26 PISQVRGDPFTEDTTPN---RVTYTSQVGLITHYLMIEVEMKEL-CNGNSDCMND 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 82 PVLVOSGNRAPETIMQEEEMRYTVSTFSG-----IPDRQKPLTCNKKRKNEMED 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 82 ALAENMLKLPETQRNDGCTGYNOETCLIKISSGLLEHYSLEYEMKNNL-KDNKKDK-- 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 134 VASAENMMNMQALRPAA--KCHQKAIL---YQDMQIQGKIDSALKSTVMSDYKNDKLT 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 139 ---ARVLRQRTETLIHIFNOE-----VKDLHKIPLTPPISN-ALLTDKLESQKEMLR 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 189 DAISLRKYLR--FTLVDAVTGEMATSPVNYEKVPLPDKNEASTDTMQIQMQLQ 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 188 KTIQIFILKS 197
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 247 KTYKAAVKDL 256
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 14
S28261
centromere protein E - human
N:Alternate names: centromere 312K protein; kinesin-related protein CENP-E
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 19-Jan-2001
C:Accession: S28261
R:Yen, T.J.; Li, G.; Schar, B.T.; Szliak, I.; Cleveland, D.W.

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OS *Sylvilagus auduboni* (desert cottontail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.
 OX NCBI_TaxID=30581;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 RT European rabbit (*Oryctolagus cuniculus*).";
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169177; AAF86661.1; -;
 DR InterPro: IPR003573; -;
 DR pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOWN_1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SO SEQUENCE 118 AA; 13763 MW; 9DDDB8C812ED31049 CRC64;

Query Match 18.7%; Score 205.5; DB 6; Length 118;
 Best Local Similarity 36.0%; Pred. No. 1.2e-10;
 Matches 41; Conservative 29; Mismatches 43; Indels 1; Gaps 1;

OY 97 DCCYOTGYNOECLIKISSGLLEHSHYLEYMKNNLK-DNKKKARVLODTEFLIHIFNQ 155
 DB 3 DCCFPLANHECTCLRTITSGLEFQMYLEHLQAKRSEEDENRVSMMLKNIRYLKTLRP 62
 OY 156 EVKDLHKIVLPPIPSNALLTDKLESQEWLRTKTIOFILKSLEEFKVTLRSTR 209
 DB 63 KVNNEGATLKPAYVASLMKNLQOKDQWLKTTTHIFILRLNLTDFLQPSLRA 116

RESULT 14
 OY9MZ08 PRELIMINARY; PRT; 118 AA.
 ID O9MZ08;
 AC O9MZ08;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS *Lepus californicus* (Black-tailed jackrabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 OX NCBI_TaxID=48087;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 RT European rabbit (*Oryctolagus cuniculus*).";
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169179; AAF86663.1; -;
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SO SEQUENCE 118 AA; 13712 MW; 3EFF24AF8D70A219 CRC64;

Query Match 18.2%; Score 199.5; DB 6; Length 118;
 Best Local Similarity 35.7%; Pred. No. 4e-10;
 Matches 40; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

OY 97 DCCYOTGYNOECLIKISSGLLEHSHYLEYMKNNLK-DNKKKARVLODTEFLIHIFNQ 155
 DB 3 DCCFPLANHECTCLRTITSGLEFQMYLEHLQAKRSEEDENRVSMMLKNIRYLKTLRP 62
 OY 156 EVKDLHKIVLPPIPSNALLTDKLESQEWLRTKTIOFILKSLEEFKVTLRSTR 207
 DB 63 KVNNEGATLKPAYVASLMKNLQOKDQWLKTTTHIFILRLNLTDFLQPSLRA 114
 RESULT 15
 OY9MZ07 PRELIMINARY; PRT; 118 AA.
 ID O9MZ07;
 AC O9MZ07;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS *Lepus townsendii* (white-tailed jackrabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Lepus.
 OX NCBI_TaxID=63225;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RX MEDLINE=20304414; PubMed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 RT European rabbit (*Oryctolagus cuniculus*).";
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169180; AAF86664.1; -;
 DR InterPro: IPR003573; -;
 DR InterPro: IPR003574; -;
 DR pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SO SEQUENCE 118 AA; 13712 MW; 3EFF24AF8D70A219 CRC64;

Query Match 18.2%; Score 199.5; DB 6; Length 118;
 Best Local Similarity 35.7%; Pred. No. 4e-10;
 Matches 40; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

OY 97 DCCYOTGYNOECLIKISSGLLEHSHYLEYMKNNLK-DNKKKARVLODTEFLIHIFNQ 155
 DB 3 DCCFPLANHECTCLRTITSGLEFQMYLEHLQAKRSEEDENRVSMMLKNIRYLKTLRP 62
 OY 156 EVKDLHKIVLPPIPSNALLTDKLESQEWLRTKTIOFILKSLEEFKVTLRSTR 207
 DB 63 KVNNEGATLKPAYVASLMKNLQOKDQWLKTTTHIFILRLNLTDFLQPSLRA 114

Search completed: October 4, 2001, 19:12:01
 Job time: 1187 sec

OS Actus nigriceps (black-headed night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.
 ON NCBI_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
 RA Patarroyo M.E.;
 RT "Actus nigriceps gene for IL-6."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF097322; AAF21297.1; -
 DR HSSP; P05231; 1ALU.
 DR InterPro; IPR002069; -
 DR InterPro; IPR003573; -
 DR InterPro; IPR003574; -
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6CSFMGF.
 DR PROSITE; PR00434; INTERLEUKIN6.
 DR PRODOM; PD002435; -; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SMART; SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 175 AA; 19205 MW; 2BCCE574CB99B189 CRC64;

Query Match 30.6%; Score 336.5; DB 6; Length 175;
 Best Local Similarity 42.4%; Pred. No. 8.3e-22;
 Matches 72; Conservative 33; Mismatches 62; Indels 3; Gaps 3;

OY 1 MKFLSARDFHVAF-LGLMLVTTTAFPTSOVRDQFTEDTTPNRPVYT-TSQVGLTHV 58
 DB 1 MNSFSTAFPRVAFSLDLLVPAAPAPVPLGDSKEVAAPNQLLTSTEQIDKHRYI 60
 OY 59 LMEIYERKEICNGNSDCMNDALAEENNLKLPRIQRNDGCGYGTGNOEICLKISSGL 118
 DB 61 LEGIALRKEICDKSNCSSEKALAEENNLNLPKMAEKDCGFCGPFNEICLKITTGL 120
 OY 119 EYHSYLEYKNNLNKDKKARVLQRTETLTHFNOEYKDKLKIYVPTP 168
 DB 121 EFVYLEYLQNR-ESSKEQAGAVQMSTKGLISLQKRNKLSIAVPPDP 169

RESULT 11
 OY97535 PRELIMINARY; PRT; 160 AA.
 ID OY97535;
 AC OY97535;
 DT 01-MAY-1999 (TEMBLrel. 10, Created)
 DT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Actus vociferans (noisy night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Actus.
 ON NCBI_TaxID=57176;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
 RT "Identification, cloning and sequencing of different Interleukin genes
 in 4 Actus species."
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF014505; AAD01531.1; -
 DR HSSP; P05231; IL6.
 DR InterPro; IPR003573; -
 DR InterPro; IPR003574; -
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6CSFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; 1.
 DR SMART; SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 160 AA; 17855 MW; 07A021338650A46D CRC64;

Query Match 28.0%; Score 307.5; DB 6; Length 160;
 Best Local Similarity 43.6%; Pred. No. 2.5e-19;
 Matches 65; Conservative 30; Mismatches 51; Indels 3; Gaps 3;

OY 1 MKFLSARDFHVAF-LGLMLVTTTAFPTSOVRDQFTEDTTPNRPVYT-TSQVGLTHV 58
 DB 1 MNSFSTAFPRVAFSLDLLVPAAPAPVPLGDSKEVAAPNQLLTSTEQIDKHRYI 60
 OY 59 LMEIYERKEICNGNSDCMNDALAEENNLKLPRIQRNDGCGYGTGNOEICLKISSGL 118
 DB 61 LEGIALRKEICDKSNCSSEKALAEENNLNLPKMAEKDCGFCGPFNEICLKITTGL 120
 OY 119 EYHSYLEYKNNLNKDKKARVLQRTETLTHFNOEYKDKLKIYVPTP 147
 DB 121 EFVYLEYLQNR-ESSKEQAGAVQMSTK 148

RESULT 12
 OY9MZ09 PRELIMINARY; PRT; 118 AA.
 ID OY9MZ09;
 AC OY9MZ09;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Sylvilagus nuttallii (mountain cottontail).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Sylvilagus.
 ON NCBI_TaxID=50378;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE=20304414; Pubmed=10843729;
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 European rabbit (Oryctolagus cuniculus)."
 RL Cytokine 12:555-565(2000).
 DR EMBL; AF169178; AAF86662.1; -
 DR InterPro; IPR003573; -
 DR InterPro; IPR003574; -
 DR Pfam; PF00489; IL6; 1.
 DR PRINTS; PR00433; IL6CSFMGF.
 DR PROSITE; PR00434; INTERLEUKIN_6; 1.
 DR PROSITE; PS00254; INTERLEUKIN_6; UNKNOWN_1.
 DR SMART; SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 118 AA; 13834 MW; 62E97FD3BDBEABEC CRC64;

Query Match 18.9%; Score 207.5; DB 6; Length 118;
 Best Local Similarity 36.8%; Pred. No. 8.1e-11;
 Matches 42; Conservative 28; Mismatches 43; Indels 1; Gaps 1;

OY 97 DGCYGTGNOEICLKISSGLLEYSYLEYKNNLNKDKKD-KARVLQRTETLTHFNO 155
 DB 3 DGCFLPAHNEICLRLTSGLEFOMYLEHQAFAFSEKENTRSMILKNRHLINLRP 62
 OY 156 EYKDLKIYVPTPISNALTDKLSQKEMLRKTIQFIKLSLEFLVTLRSTR 209
 DB 63 KVKNFNGVTLKPAIVASLMEINLQKQDWLKMPTIHLRCLTDFLQFLASVR 116

RESULT 13
 OY9MZRO PRELIMINARY; PRT; 118 AA.
 ID OY9MZRO;
 AC OY9MZRO;
 DT 01-OCT-2000 (TEMBLrel. 15, Created)
 DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.

OX NCBI_TaxID=10029;
 RN
 RP SEQUENCE FROM N.A.
 RA Helene H., Delude R.D., Monks B., Golenbock D.T.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF044667; AAC02100.1; -.
 DR HSSP: P05231; 1ALU.
 DR InterPro: IPR003573; -.
 DR Pfam: PF00489; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 FT NON_TER 101
 SO SEQUENCE 101 AA; 11749 MW; 2923BC259C49A974 CRC64;

Query Match 33.1%; Score 372; DB 11; Length 101;
 Best Local Similarity 70.7%; Pred. No. 3.6e-25;
 Matches 70; Conservative 14; Mismatches 15; Indels 0; Gaps 0;

QY 93 IORNGCYOTGYNOEICLLKISSGLLEHYSHYLYEYKNNLKKDKKARVYQDTEFLIH 152
 DB 2 IORNGCYOTGYNWEICLLKISSGLLDYQYILEFTNNVQDKKARVYQDTEFLISQI 61
 QY 133 FNOEYKDLHKIVLPPISSNALLTDKLESOKEMLRRTKIQ 191
 DB 62 FNOEYKDPKIVMPSPTSKAILERLESOKQMPRTKIE 100

RESULT 8
 Q28403 PRELIMINARY: PRT; 207 AA.
 AC Q28403;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Euhadra luteira (Sea otter).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Euhydra.
 OX NCBI_TaxID=34882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-96163018; PubMed-8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidsdson T.H., Hanni K.D.,
 RA Stolt J.L., Perlick D.A.;
 RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
 RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Euhadra luteira nereis).";
 RL Immunogenetics 43:190-195(1996).
 DR EMBL: L46804; AA01428.1; -.
 DR HSSP: P05231; IL6.
 DR InterPro: IPR003573; -.
 DR InterPro: IPR003574; -.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFPMF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 FT NON_TER 101
 SO SEQUENCE 207 AA; 23527 MW; 729EBC0D91136D8B CRC64;

Query Match 33.1%; Score 363.5; DB 6; Length 207;
 Best Local Similarity 38.8%; Pred. No. 4.6e-24;
 Matches 81; Conservative 48; Mismatches 71; Indels 9; Gaps 5;

QY 5 SARDEHPVAF-IGLMVTTAAPTSGVRGDFETDTPNRPVYTS-QVGLITHVLEWEI 62
 DB 2 STSASPVAFSGLLVMTAAPTSGVRLGDSKSDATSNRPPLTSADKMEDEFIKIKRI 61
 QY 63 VEMKRELCSGNDGNNNDALAEENNLKLPFIQRNDCYOTGYNOEICLLKISSGLLEHYS 122

DB 62 SALRNMCDKYNKCEDSKSEVLAEENNLKLPKLAEXRCFCFSFRENQETCLRTITGLOEFOI 121
 QY 123 YLEVKNNLKKDKKARVYQDTEFLIHFNQEVKDLHKI--VLPPISSNALLTDKLES 180
 DB 122 HLKYLESNTEG-KDNASVYISTKHL---QTLRPMNOIEVTPDPPTDASIALKFS 176
 QY 181 QKEMLRRTKIQFILKSLSEFLKVTLRSTR 209
 DB 177 QDKMLKHTTHILRLRDLDFQFSLRATR 205

RESULT 9
 Q9MZRL PRELIMINARY: PRT; 241 AA.
 AC Q9MZRL;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN 6.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE-SPLEEN, LYMPH NODE;
 RX MEDLINE-20304414; PubMed-10843729;
 RA Perlins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
 RT European rabbit (Oryctolagus cuniculus).";
 RL Cytokine 12:555-565(2000).
 DR EMBL: AF169176; AAF66660.1; -.
 DR InterPro: IPR003573; -.
 DR InterPro: IPR003574; -.
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFPMF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; UNKNOMN_1.
 DR SMART: SM00126; IL6; 1.
 SO SEQUENCE 241 AA; 27021 MW; 781D323692C3EE97 CRC64;

Query Match 31.0%; Score 340.5; DB 6; Length 241;
 Best Local Similarity 36.6%; Pred. No. 5.4e-22;
 Matches 71; Conservative 42; Mismatches 80; Indels 1; Gaps 1;

QY 15 IGLMVTTAAPTSGVRGDFETDTPNRPVYTSQVGLITHVLEIYEMKRELCSGNS 74
 DB 17 LALLLVATAAPTSGAPVRSDSNWKASPDCTLTPPGRTIESIRSIETIKELRKEMCDHDV 76
 QY 75 DCMNNDALAEENNLKLPFIQRNDCYOTGYNOEICLLKISSGLLEHYSHYLYEYKNNL-K-D 133
 DB 77 NCMNREKALAEVNLHPLRIEDGCPPAVNVNNEICLRTTSGLMERMYLEHLQKPFSD 136
 QY 134 NKDKARVYQDTEFLIHFNQEVKDLHKIVLPPISSNALLTDKLESOKEMLRRTKIQFI 193
 DB 137 EENTRYSVNLKNQILKLRPKVKNLNEAVLKPAVAVSLMENLQKNQWMLKTTIHFI 196
 QY 194 LKSLSEFLKVTLSR 207
 DB 197 LRGLTNFLEFLTRA 210

RESULT 10
 Q9TTH4 PRELIMINARY: PRT; 175 AA.
 AC Q9TTH4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.

Db 61 IYELRKLCCNNPNCMDNDVLLNNLELPIVQINDGLQGTGYNMEICLLKITSGLIDYQ 120
 QY 122 SYLEWMKNNLKDKKKDKARVLOQDTELLHIFNOEYKDLIVLPPISSNALLTKLESQ 181
 Db 121 IYLEEVTNNVQNNKKDKARVIOSTIKTISQITKQEKYKGDKITVTSPTSKALIMKLESQ 180
 QY 182 KEMLRKTIQIQLKSLEFLKVTLRSTQ 210
 Db 181 KEMPRKTIKILKALEEFLVETMRSTQ 209

RESULT 2

QJHH3 PRELIMINARY: PRT: 207 AA.

AC QJHH3;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuriidae; Sciurinae;
 OC Marmota.
 OC NCBI_TaxID=9995;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Li D.H., Cullen J.M.;
 RL "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis."
 RL Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li D.H., Cullen J.M.;
 RT "Gene Structure of the Woodchuck Interleukin-6."
 RT Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF012908; AAF34861.1;
 DR EMBL: AF122896; AAF28873.1;
 DR InterPro: IPR003573;
 DR InterPro: IPR003574;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA; 23645 MW; AD2F46E450E13470 CRC64;

Query Match 44.0%; Score 483; DB 11; Length 207;
 Best Local Similarity 44.8%; Pred. No. 2e-34;

Matches 95; Conservative 47; Mismatches 62; Indels 8; Gaps 3;

QY 1 MKFLSARDHPHAF-IGLMVYTTTAPTSQVRRGDFTEPTTNR-PVITTSQVGLITIV 59
 Db 1 MKFFS-----IASGGLLVAFAPASLOREDEGNSVTRKPPRASGKTAGOISYLI 54
 QY 60 WEIVEMRKELCNGNSDCNNNDALAEENNLKLPETIORNDGCTGYNOEICLKITSGL 119
 Db 55 KEVFEKRLCKNDDETCISHVAVSNNNLNPKMTEKDCDGFOTGYRNDGIVRTISGLLE 114
 QY 120 YHSYLEYMKNNLK-D-NKKDKARVLOQDTELLHIFNOEYKDLHKLIVLPPISSNALLTKRL 178
 Db 115 FOVYIAYIRNKKFOEGNNRRAEHVOFSKALILEIKOEYKDPNKIVFPSPNTINILAKL 174
 QY 179 ESQKEWLRKTIQIQLKSLEFLKVTLRSTQ 210
 Db 175 ESQNDQKVTMQLILSNEDFLQFTLRVRK 206

RESULT 3

QJHH3 PRELIMINARY: PRT: 209 AA.

ID QJ7540
 AC QJ7540;
 DT 097540;
 DT 097540;
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus nancymae (Owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=37293;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
 RT "Identification, cloning and sequencing of different interleukin genes
 in 4 Aotus species."
 RT Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF014510; AAD01536.1;
 DR HSSP: P05231; IAUU.
 DR InterPro: IPR003573;
 DR SMART: SM00126; IL6; 1.
 DR NON_TER 1
 FT NON_TER 209 209
 SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus nancymae (Owl monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBI_TaxID=37293;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Echeverry S.J., Hernandez E., Moreno A., Patarroyo M.E., Murillo L.A.;
 RT "Identification, cloning and sequencing of different interleukin genes
 in 4 Aotus species."
 RT Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF014510; AAD01536.1;
 DR HSSP: P05231; IAUU.
 DR InterPro: IPR003573;
 DR InterPro: IPR003574;
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 DR NON_TER 1
 FT NON_TER 209 209
 SQ SEQUENCE 209 AA; 23406 MW; E84F085DD84002DD CRC64;

Query Match 38.9%; Score 427.5; DB 6; Length 209;
 Best Local Similarity 42.6%; Pred. No. 1.3e-29;

Matches 89; Conservative 43; Mismatches 74; Indels 3; Gaps 3;

QY 1 MKFLSARDHPHAF-IGLMVYTTTAPTSQVRRGDFTEPTTNR-PVITTSQVGLITIV 58
 Db 1 MNSFSSARFPAFSGILLVMPAFAPVPGEDSKFEVAAENRQPLSTEDIDKHRYI 60
 QY 59 LWEIVEMRKELCNGNSDCNNNDALAEENNLKLPETIORNDGCTGYNOEICLKITSGL 118
 Db 61 LDGIALRKRETCNKSMMCSSKEALAEENNLNPKMAEKGGCOSCQFNETCLVKIITGL 120
 QY 119 EYHSYLEYMKNNLKDKKKARVLOQDTELLHIFNOEYKDLHKLIVLPPISSNALLTKRL 178
 Db 121 EEEVYLEYLQNR-ESSEEQARAVQSTVLIQLOKKAKNDAITTPPTTNASILTKL 179
 QY 179 ESQKEWLRKTIQIQLKSLEFLKVTLRSTQ 207
 Db 180 QAQNMQLQDTHLILRSKFLQSSLA 208

RESULT 4
 QJHH3 PRELIMINARY: PRT: 208 AA.

AC QJX780;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE INTERLEUKIN 6 PRECURSOR
 OS Delphinapterus leucas (beluga whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
 OC Monodontidae; Delphinapterus.
 OC NCBI_TaxID=9749;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
 RT "Molecular cloning and phylogenetic analysis of beluga whale
 (Delphinapterus leucas) Interleukin 6."
 RT Submitted (JUL-1998) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF076643; AAD42929.1;
 DR HSSP: P05231; IAUU.
 DR InterPro: IPR003573;
 DR InterPro: IPR003574;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:12:00 ; Search time 74.43 Seconds
(Without alignments)
375,069 Million cell updates/sec

Title: US-09-230-048-4
Sequence: 1 MKFLSARDFHPVAFGLMLV.....FILSKLEFLKVTLSRNOT 211

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_PROTOCT:*
12: SP_UNCLASSIFIED:*
13: SP_VIRIDATE:*
14: SP_VIRUS:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	774.5	70.5	210	11	Q9WVQ8
2	483	44.0	207	11	Q9JH13
3	427.5	38.9	209	6	O97540
4	420	38.3	208	6	O9XW80
5	411.5	37.5	209	6	O9TTH3
6	402	36.6	207	6	O9WZ27
7	372	33.9	101	11	O55041
8	363.5	33.1	207	6	O28403
9	340.5	31.0	241	6	O9MZK1
10	336.5	30.6	175	6	O9TTH4
11	307.5	28.0	160	6	O97535
12	207.5	18.9	118	6	O9WZ09
13	205.5	18.7	118	6	O9MZK0
14	199.5	18.2	118	6	O9MZK8
15	199.5	18.2	118	6	O9MZK7
16	199.5	18.2	115	6	O9MZK5
17	150	13.7	204	14	O40918
18	148	13.5	204	14	O98823
19	147.5	13.4	94	6	O62775

20	103	9.4	977	5	O9U0H9	O9U0H9 plasmodium
21	96	8.7	196	11	O9EQ14	O9eq14 mus musculu
22	96	8.7	819	5	O93228	O93228 caenorhabdi
23	95	8.7	3325	14	O91BT9	O91bt9 turkey herp
24	95	8.7	3342	14	O9E6N3	O9ebn3 turkey herp
25	93.5	8.5	1354	6	O77819	O77819 oryctolagus
26	90.5	8.2	1127	14	O91VT6	O91vt6 melanoplus
27	90.5	8.2	2042	5	O25766	O25766 plasmodium
28	88.5	8.1	553	5	O9VKZ2	O9vK22 drosophila
29	88.5	8.1	826	5	O9N894	O9n894 plasmodium
30	88	8.0	421	10	O9LX20	O9lX20 arabis
31	87.5	8.0	643	5	O9VAC1	O9vAc1 drosophila
32	87	7.9	421	10	P92952	P92952 arabidopsis
33	86.5	7.9	460	10	O9SHQ0	O9shq0 arabidopsis
34	86.5	7.9	645	2	O07869	O07869 streptococ
35	86.5	7.9	743	10	O9ZVX5	O9zVx5 arabidopsis
36	86.5	7.9	768	5	O9NAX6	O9nAx6 dictyostell
37	86.5	7.9	823	4	O9H0H6	O9h0H6 homo sapien
38	85.5	7.8	1516	5	O96154	O96154 plasmodium
39	85	7.7	189	4	O9H2A5	O9h2A5 homo sapien
40	85	7.7	1098	2	O9R2W8	O9r2W8 borrelia bu
41	85	7.7	2771	5	O26216	O26216 plasmodium
42	84.5	7.7	207	14	O9EMR7	O9emr7 amasacta moo
43	84.5	7.7	1156	2	O66878	O66878 aquifex aeo
44	84	7.7	189	4	O9NPF7	O9nPF7 homo sapien
45	84	7.7	636	2	O51624	O51624 borrelia bu

ALIGNMENTS

RESULT	1	PRELIMINARY;	PRT;	210 AA.
Q9WVQ8	O9WVQ8			
AC	O9WVQ8			
DT	01-NOV-1999 (TREMURel. 12, Created)			
DT	01-NOV-1999 (TREMURel. 12, Last sequence update)			
DT	01-MAR-2001 (TREMURel. 16, Last annotation update)			
DE	IL-6 (FRAGMENT).			
OS	Mesocricetus auratus (Golden hamster).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;			
OC	Mesocricetus.			
OX	NCBI_TaxID=10036;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPRAIN-APA; TISSUE-KIDNEY;			
RA	Nishida E.;			
RT	"APA hamsters IL-6 partial cDNA."			
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AB028635; BAA78766.1; -			
DR	HSSP; P05231; 1ALU.			
DR	InterPro; IPR003573; -			
DR	InterPro; IPR003574; -			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PR00433; IL6GSGFWGF.			
DR	PRINTS; PR00434; INTERLEUKIN6.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
DR	SMART; SM00126; IL6; 1.			
FT	NON_TER			
SO	SEQUENCE	210 AA;	24060 MW;	BD9319AFB913AB3 CRC64;

Query Match 70.5%; Score 774.5; DB 11; Length 210;

Best Local Similarity 72.7%; Pred. No. 1e-59; Matches 15; Conservative 22; Mismatches 34; Indels 1; Gaps 1;

OY	3	FLSARDFHPVAFGLMLVTTTAFPTQVRRGDTEDTTPNRPVYTTS-QVGGILTHVLM	61
OY	1	FLSARDFHPVAFGLMLVTTTAFPTQVRRGDTEDTTPNRPVYTTS-QVGGILTHVLM	60
OY	62	IVERRKELCKNSCCANNDALAEENIKLPEIQANDCGYOTGVNOETCLLKISSGLETH	121


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CC -----
DR EMBL: L26028; AAA9978.1; -
DR HSSP; P05231; 1ALU.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFNGF.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
DR SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23728 MM; 4130DEOCFOBCAD CRC64;

Query Match 37.5%; Score 411.5; DB 1; Length 212;
Best Local Similarity 40.1%; Pred. No. 3e-27;
Matches 85; Conservative 48; Mismatches 76; Indels 3; Gaps 3;

OY 1 MKFLSARDFHPYAF-IGMLVTTTAFPTSOVARGDFTDTP-NRPVYTSQVGLITHV 58
DB 1 MNSFTSAFPGVAFSLGLLVLPAPFAPVLPBGEDSKVAAPHSPVLTSSERIDKHIRY 60
OY 59 LWEIEMKREKLCNGSDCMNDALAEENNLKLPETORNDGCGYGTGNOEICILKISSGL 118
DB 1 LGISALRKKEKCMNDYMKCKDSKEALAEENNLKPKAEKDGCGSFNEDTCLRTITGL 120
OY 119 EYHSLLEYMKNNKDKKDKARVLDRTETLIHFNOEKDLHKVLPPTISNALLTDKL 178
DB 121 EEEVLEFLQDNF-ESSEQAAVOMSTKVLIQFLQKRAKMLDAITTEPTNASLITKL 179
OY 179 ESQKEMLRKTIOFIKLSLEFLKVTLRSTRO 210
DB 180 QAQNMQLDMTHLILRSFKFLOSLNALRQ 211

RESULT 15
IL6_FELCA STANDARD; PRT; 208 AA.
AC PA1683;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Fells sivestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX NCBI_TaxID:9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94162386; Pubmed=8117820;
RA Ohashi T., Matsumoto Y., Watari T., Gotsuka R., Tsujimoto H.,
RA Hasegawa A.;
RT "Molecular cloning of feline interleukin-6 cDNA.";
RL J. Vet. Med. Sci. 55:941-944(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymphocytes;
RX MEDLINE=94052249; Pubmed=8234373;
RA Birdley W.G., Gibbs C., Kraus L., Good R.A., Day N.K.;
RT "Molecular cloning and characterization of a cDNA encoding feline
interleukin-6.";
RL Proc. Soc. Exp. Biol. Med. 204:301-305(1993).
CC -!- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.

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CC -----
DR EMBL: L16914; AAA16620.1; -
DR EMBL: D13227; BAA02507.1; -
DR HSSP; P05231; 2IL6.
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; 1.
DR PRINTS; PR00433; IL6GCSFNGF.
DR PROSITE; PS00254; INTERLEUKIN_6; 1.
DR Cytokine; Glycoprotein; Growth factor; Signal.
DR SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 208 INTERLEUKIN-6.
FT DISULFID 68 74 BY SIMILARITY.
FT DISULFID 97 107 BY SIMILARITY.
FT CONFLICT 2 2 T->N (IN REF. 2).
FT CONFLICT 45 45 S->P (IN REF. 2).
FT CONFLICT 133 133 E->K (IN REF. 2).
FT CONFLICT 173 187 AKLOSQEWMLRHTTI->LSCSHRVAEAHNN (IN
REF. 2).
FT CONFLICT 200 201 FS->LR (IN REF. 2).
SQ SEQUENCE 208 AA; 23401 MM; 93B4456B298C6AC CRC64;

Query Match 36.6%; Score 401.5; DB 1; Length 208;
Best Local Similarity 38.9%; Pred. No. 2e-26;
Matches 82; Conservative 51; Mismatches 71; Indels 7; Gaps 4;

OY 1 MKFLSARDFHPYAF-IGMLVTTTAFPTSOVARGDFTDTPNRPVYTSQVGLITHV 58
DB 1 MFLSTSAFSPPLAFSLGLLVATAFPFP---GFLGSDATSNRLPLTSADKMEELIYI 56
OY 59 LWEIEMKREKLCNGSDCMNDALAEENNLKLPETORNDGCGYGTGNOEICILKISSGL 118
DB 57 LGISALRKKEKCMNDYMKCKDSKEALAEENNLKPKAEKDGCGSFNEDTCLRTITGLQ 116
OY 119 EYHSLLEYMKNNKDKKDKARVLDRTETLIHFNOEKDLHKVLPPTISNALLTDKL 178
DB 117 EFGIYLFQDNF-EGDENAKSVYTSNVLQMLKRGKNDDEVITIPVYEVGLQAKL 175
OY 179 ESQKEMLRKTIOFIKLSLEFLKVTLRSTR 209
DB 176 OSQEWMLRHTTIHLTLRLRLDFLOPSLRAVR 206

Search completed: October 4, 2001, 19:12:35
Job time: 270 sec

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RESULT 13
ID IL6_PROV1 STANDARD: PRT: 209 AA.
AC Q28819;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
OS IL6.
OS Phoca vitulina (Harbor seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Plinnipedia; Phocidae; Phoca.
OX NCBI:"taxid=9720;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96163018; Pubmed=8575617;
RA King D.P., Schrenzel M.D., McKnight M.L., Reldarson T.H., Hanni K.D.,
RA Scott J.L., Perrick D.A.;
RT "Molecular cloning and sequencing of interleukin 6 cDNA fragments from
RT the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
RT Southern sea otter (Enhydra lutris nereis).";
RL Immunogenetics 43:190-195(1996).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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RESULT 14
ID IL6_MACMU STANDARD: PRT: 212 AA.
AC P51494;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithechinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP STRAIN=MAC 2.
RP SEQUENCE FROM N.A.
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC -----
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DR PRINTS: PR00433; IL6GCSFMC.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PRINTS: PS00254; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6.
DR CYTOKINE: Glycoprotein; Growth factor; Signal.
KM CYTOKINE: Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 208 INTERLEUKIN-6.
FT DISULFID 72 78 BY SIMILARITY.
FT DISULFID 101 111 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 4 4 L-> R (IN REF. 2).
FT CONFLICT 110 110 I-> V (IN REF. 2).
FT CONFLICT 171 171 M-> L (IN REF. 2).
FT CONFLICT 201 201 S-> R (IN REF. 2).
SQ SEQUENCE 208 AA; 23446 MW; EEC96C13E3230A0 CRC64;

Query Match
Best Local Similarity 38.2%; Score 419.5; DB 1; Length 208;
Matches 86; Conservative 47; Mismatches 71; Indels 7; Gaps 4;

OY 1 MKFLSARDFHPVAF-LGLMLVTTTAPPTSOVRGDFTEEDTTPRPVYTT-SOVGGLITHV 58
DB 1 MNSLFTSAFSPVAFSGLLVMTSAFPTPGLEGDEKNTTTSRLTLTPKTEALIKHI 60
OY 59 LMEIYEMKRELONGSDCNDNDALAENNLKLPETQRNDGQYGTGYNOEICLTKISSGL 118
DB 61 IKGISALRRETCNRSNMCESSKEALAEENNLKPKMEKDCGCSGFNDCTLVKIIITGL 120
OY 119 EYHSYLEVKKNNLKNKKKARAVLQDFTETLIHFNOEKDLHKIVLPPTISNALLTDKL 178
DB 121 EYQIYLDPLQNFPEGN-QETVMELOSITFTLIQILKEKTAGL---ITTPATHTDMLERM 175
OY 179 ESQKEMLRRTTQIOTILKSLEFLKAVTLRSTR 209
DB 176 QSSNEWKNAKXIIILRSLENFLQPSLRAIR 206

RESULT 11
IL6_MACFA STANDARD; PRT: 212 AA.
AC P79341:
DR 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Macaca fascicularis (Crap eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_Taxid=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Tatum M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: AB000554; BAA19148.1;
CC DR HSSP: P05231; 2IL6.
CC DR InterPro: IPR001716;

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DR Pfam: PF00489; IL6; 1.
DR PRINTS: PR00433; IL6GCSFMC.
DR PRINTS: PR00434; INTERLEUKIN6.
DR PROSITE: PS00254; INTERLEUKIN6.
DR CYTOKINE: Glycoprotein; Growth factor; Signal.
KM CYTOKINE: Glycoprotein; Growth factor; Signal.
FT SIGNAL 1 29 BY SIMILARITY.
FT CHAIN 30 212 INTERLEUKIN-6.
FT DISULFID 72 78 POTENTIAL.
FT DISULFID 101 111 POTENTIAL.
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 212 AA; 23654 MW; CF8173FCHF0B0389 CRC64;

Query Match
Best Local Similarity 37.8%; Score 415.5; DB 1; Length 212;
Matches 85; Conservative 51; Mismatches 73; Indels 3; Gaps 3;

OY 1 MKFLSARDFHPVAF-LGLMLVTTTAPPTSOVRGDFTEEDTTP-NRPVYTTSOVGLITHV 58
DB 1 MNSVSTSAFSPVAFSGLLVLPAPVLPGEESKDVAAPHSGPLTSERIDKHIXI 60
OY 59 LMEIYEMKRELONGSDCNDNDALAENNLKLPETQRNDGQYGTGYNOEICLTKISSGL 118
DB 61 IKGISALRRETCNRSNMCESSKEALAEENNLKPKMEKDCGCSGFNDCTLVKIIITGL 120
OY 119 EYHSYLEVKKNNLKNKKKARAVLQDFTETLIHFNOEKDLHKIVLPPTISNALLTDKL 178
DB 121 EYEVILEYQNF-ESSEQANAVOMSTKVLIQIOLKAKKALIDAITTPEPTTNASLTKL 179
OY 179 ESQKEMLRRTTQIOTILKSLEFLKAVTLRSTRO 210
DB 180 QAQNMWLODMTHLLRSFKEFLQSSLRALRQ 211

RESULT 12
IL6_CERTO STANDARD; PRT: 212 AA.
AC P46650:
DR 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE INTERLEUKIN-6 PRECURSOR (IL-6).
GN IL6.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_Taxid=9531;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-96003435; PubMed-7561102;
RA Villinger F.J., Brar S.S., Wayne A.E., Chikala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
J. Immunol. 155:3946-3954(1995).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC -----
CC EMBL: L26032; AAA9972.1;
CC DR

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Query Match 38.3%; Score 420.5; DB 1; Length 212;
 Best Local Similarity 41.8%; Pred. No. 5.5e-28;
 Matches 89; Conservative 50; Mismatches 69; Indels 5; Gaps 5;

DB 1 MKPISADPHVAF-LGLMLVTTTAFPPSOVRKDFED-TTPNR-PVYTTSQVGLITH 57
 1 MNSFSTAFGVAFSLGLLVLPAAFP-APVPPGEDSKDVAAHPROPLTSSERIDKOIRY 59
 58 VLMEIVEMREKLNGNSDCMNNDALENKLPFIQRNDGCGYGYNOEICLIKISSGL 117
 60 ILDCISLRKTKCKSNKSCSSKALAEENNLKPKMAEKDCGCGFNGETCLVKITITGL 119
 118 LEVHSYLEYKNNLNKDKKARVLQRDTETLHIFNQEVKDLHKIVLPTPISNALLTDK 177
 120 LEFEVYLEYLQNR-ESSEQARAVQSTKVLQFLQKKKNLDAITTPDPTNASLLTK 178
 178 LESQEWLRKTKTIOPIILKSLKEEFLKVLTRSTRQ 210
 179 LQAQNMLODMTHILIRSEFEFLQSSLRALRQ 211

RESULT 9
 IL6_ORCOR STANDARD; PRT; 205 AA.
 AC Q28747;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6) (FRAGMENT).
 GN IL6.
 OS Orcinus orca (Killer whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
 OC Orcinus.
 OC NCBI_TaxID=9733;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Scott J.L., Forrick D.A.;
 RT "Molecular cloning and sequencing of Interleukin 6 cDNA fragments from
 the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 RT Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; LA6803; AAB01429.1; .
 CC HISSP; P05231; IALU.
 CC InterPro: IPR001716; .
 CC Pfam: PF00489; IL6; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 KW Cytokine; Glycoprotein; Growth factor; Signal.
 FT SIGNAL 1
 FT NON_TER 1
 FT CHAIN 21 21 BY SIMILARITY.
 FT DISULFID 22 205 INTERLEUKIN-6.
 FT 64 70 BY SIMILARITY.
 FT DISULFID 93 103 BY SIMILARITY.

FT CARBOHYD 164 164 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 205 AA; 23266 MW; 6308F3A457960832 CRC64;
 Query Match 38.2%; Score 419.5; DB 1; Length 205;
 Best Local Similarity 43.9%; Pred. No. 6.4e-28;
 Matches 87; Conservative 42; Mismatches 64; Indels 5; Gaps 4;

DB 15 LGLMLVTTTAFPPSOVRKDFEDTTPNRPVYTS--QVGLITHVLMEIYEMREKELNG 72
 8 LGLLVLTATNFTPTGPRGDEPKDITSDR-LYLSPKTEALIKYILGKISARKKECEK 66
 73 NSDCMNNDALENKLPFIQRNDGCGYGYNOEICLIKISSGLBYHSYLEYKNNLNK 132
 67 YDKCENSKALAEENNLKPKMAEKDCGCGFNGETCLMRTITGLLEYQYLYDLQNEY- 125
 133 DNKKARVLQRDTETLHIFNQEVKDLHKIVLPTPISNALLTDKLESOR-EMLRRTIQ 191
 126 EGDKEALAEAVQISSKALAQILROKVNKPDEVTPDPTTNASLNILQSDNDMMKNKRII 185
 192 FILKSLKEEFLKVLTRSTR 209
 186 LILRSLENFLQFSRLAIR 203

RESULT 10
 IL6_SHEEP STANDARD; PRT; 208 AA.
 AC P29455;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94041419; PubMed=8225400;
 RA Andrews A.E., Barcham G.J., Ashman K., Meeusen E.N.T., Brandon M.R.,
 RA Nash A.D.;
 RT "Molecular cloning and characterization of a ruminant Interleukin-6
 RT cDNA";
 RL Immunol. Cell Biol. 71:341-348(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ebrahimi B.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 FUNCTIONS: IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
 OF B-CELLS INTO IG-SECRETING CELLS. IT INDUCES MYELOMA AND
 CC PLASMACTOMA GROWTH. IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
 CC -----
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 CC -----
 CC EMBL; X62501; CAA44363.1; .
 CC EMBL; X68723; CAA48662.1; .
 CC EMBL; A19159; CAA01443.1; .
 CC PIR; S29549; S29549.
 DR HISSP; P05231; 2IL6.
 DR InterPro: IPR001716; .
 DR Pfam; PF00489; IL6; 1.

RT *Structure and expression of cDNA and genes for human
RT interferon-beta-2, a distinct species inducible by growth-stimulatory
RT cytokines.";
RL EMBL J. 5:2529-2537(1986).
RN [15]
RP SEQUENCE FROM N.A.
RX MEDLINE-86088768; PubMed-3320204;
RA Brekenhoff J.P.J., de Groot E.R., Evers R.F., Pannekoek H.,
RA Aarden L.A.;
RT "Molecular cloning and expression of hybridoma growth factor in
RT Escherichia coli.";
RL Eur. J. Immunol. 139:4116-4121(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-89391958; PubMed-2789513;
RA Tonouchi N., Miwa K., Karasuyama H., Matsui H.;
RT "Deletion of 3' untranslated region of human RSP-2 mRNA causes
RT stabilization of the mRNA and high-level expression in mouse NIH3T3
RT cells.";
RL Biochem. Biophys. Res. Commun. 163:1056-1062(1989).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE-Fibroblast;
RC MEDLINE-87004683; PubMed-3758081;
RA Heegeman G., Content J., Volckaert G., Derynck R., Tavernier J.,
RA Flets W.;
RT "Structural analysis of the sequence coding for an inducible 26-kDa
RT protein in human fibroblasts.";
RL Eur. J. Biochem. 159:625-632(1986).
RN [8]
RP SEQUENCE FROM N.A.
RX MEDLINE-8919317; PubMed-3266463;
RA Wong G., Witek-Glanoff J., Hewick R., Clark S., Ogawa M.;
RT "Interleukin 6: identification as a hematopoietic colony-stimulating
RT factor.";
RL Behring Inst. Mitt. 83:40-47(1988).
RN [9]
RP SEQUENCE FROM N.A.
RX MEDLINE-93178270; PubMed-1291290;
RA Chen Q.Y.;
RT "Stable and efficient expression of human interleukin-6 cDNA in
RT mammalian cells after gene transfer.";
RL Chung-Hua Chung Liu Tsa Chih 14:340-344(1992).
RN [10]
RP SEQUENCE OF 30-63.
RX MEDLINE-88154445; PubMed-3279116;
RA van Damme J., van Beeumen J., Decock B., van Snick J., de Ley M.,
RA Billiau A.;
RT "Separation and comparison of two monokines with
RT lymphocyte-activating factor activity: IL-1 beta and hybridoma growth
RT factor (HGF). Identification of leukocyte-derived HGF as IL-6.";
RL J. Immunol. 140:1534-1541(1988).
RN [11]
RP SEQUENCE OF 50-212 OF RECOMBINANT FORM LACKING 1ST DISULFIDE BOND.
RX MEDLINE-95154344; PubMed-7851440;
RA Breton J., la Flitza A., Bertolero F., Orsini G., Valassina B.,
RA Ziliotto R., de Philippis V., Polverino de Laureto P., Fontana A.;
RT "Structure, stability and biological properties of a N-terminally
RT truncated form of recombinant human interleukin-6 containing a single
RT disulfide bond.";
RL Eur. J. Biochem. 227:573-581(1995).
RN [12]
RP DISULFIDE BONDS.
RX MEDLINE-89286115; PubMed-2472117;
RA Clogston C.L., Boone T.C., Crandall B.C., Mendiaz E.A., Lu H.S.;
RT "Disulfide structures of human interleukin-6 are similar to those of
RT human granulocyte colony stimulating factor.";
RL Arch. Biochem. Biophys. 272:144-151(1989).
RN [13]
RP MUTAGENESIS.
RX MEDLINE-91243808; PubMed-2037043;
RA Luetticken C., Kneutgen A., Moeller C., Heinrich P.C., Rose-John S.;
RT "Evidence for the importance of a positive charge and an

RT alpha-helical structure of the C-terminus for biological activity of
RT human IL-6.";
RL FEBS Lett. 282:265-267(1991).
RN [14]
RP STRUCTURE BY NMR.
RX MEDLINE-96134845; PubMed-8555185;
RA Nishimura C., Watanabe A., Gonda H., Shimada I., Arata Y.;
RT "Folding topologies of human interleukin-6 and its mutants as studied
RT by NMR spectroscopy.";
RL Biochemistry 35:273-281(1996).
RN [15]
RP STRUCTURE BY NMR.
RX MEDLINE-97303053; PubMed-9159484;
RA Xu G.-Y., Yu H.-A., Hong J., Stahl M., McDonagh T., Kay L.E.,
RA Cumming D.A.;
RT "Solution structure of recombinant human interleukin-6.";
RL J. Mol. Biol. 268:468-481(1997).
RN [16]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE-97224126; PubMed-9118960;
RA Somers W., Stahl M., Seehra J.S.;
RT "1.9-A crystal structure of interleukin 6: implications for a novel
RT mode of receptor dimerization and signaling.";
RL EMBL J. 16:989-997(1997).
CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
CC FUNCTIONS. IT PLAYS AN ESSENTIAL ROLE IN THE FINAL DIFFERENTIATION
CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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CC
DR EMBL: X04430; CAA28026.1; -
DR EMBL: M14584; AAA52728.1; -
DR EMBL: X04602; CAA28268.1; -
DR EMBL: Y00081; CAA68278.1; -
DR EMBL: M18403; AAA52729.1; -
DR EMBL: M29150; AAA59154.1; -
DR EMBL: X04402; CAA27990.1; -
DR EMBL: X04403; CAA27991.1; -
DR EMBL: M54894; AAC41704.1; -
DR EMBL: S56892; AADI3886.1; -
DR EMBL: A09363; CAA00839.1; -
DR PIR: A32648; IVHUB2.
DR PIR: A25921; A25921.
DR PDB: 1IL6; 04-FEB-98.
DR PDB: 21L6; 04-FEB-98.
DR PDB: 1ALU; 03-JUN-98.
DR MIM: 147620; -
DR InterPro: IPR001716; -
DR Pfam: PF00489; IL6; -
DR PRINTS: PR00434; IL6GCSPMGF.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
KW Cytokine; Glycoprotein; Growth factor; Signal; 3D-structure.
KW SIGNAL
FT CHAIN 1 29
FT DISULFID 30 212 INTERLEUKIN-6.
FT DISULFID 72 78
FT DISULFID 101 111
FT CARBOHYD 73 73
FT MUTAGEN 173 173 N-LINKED (GLCNAc...).
FT MUTAGEN 185 185 A->V: ALMOST NO LOSS OF ACTIVITY.
FT MUTAGEN 204 204 W->R: NO LOSS OF ACTIVITY.
FT MUTAGEN 210 210 S->P: 13% ACTIVITY.
FT MUTAGEN 212 212 R->K,E,O,T,A,P: LOSS OF ACTIVITY.
FT SEQUENCE 212 AA: 23718 MW: 17512 Da
FT M->T,N,S,R: LOSS OF ACTIVITY.
FT IFFEDFEIB734079 CRC64;

"DNA rearrangement and constitutive expression of the interleukin 6 gene in a mouse plasmacytoma.";
 RT J. Exp. Med. 171:965-970(1990).
 RN [7]
 RP SEQUENCE OF 25-211:
 RX MEDLINE-88329059; PubMed-3262059;
 RA Simpson R.J., Moritz R.L., Rubira M.R., van Snick J.;
 RT "Murine hybridoma/plasmacytoma growth factor. Complete amino-acid
 RT sequence and relation to human interleukin-6.";
 RL Eur. J. Biochem. 176:187-197(1988).
 RN [8]
 RP SEQUENCE OF 66-75; 78-84 AND 128-148.
 RX MEDLINE-90147691; PubMed-2302197;
 RA Jahnke W., Ward L.D., Reid G.E., Moritz R.L., Simpson R.J.;
 RT "Internal amino acid sequencing of proteins by in situ cyanogen
 RT bromide cleavage in polyacrylamide gels.";
 RL Biochem. Biophys. Res. Commun. 166:139-145(1990).
 RN [9]
 RP SEQUENCE OF 25-45.
 RX MEDLINE-87092311; PubMed-2948184;
 RA van Snick J., Cayphas S., Vink A., Uytendhoe C., Coule P.G.,
 RA Rubira M.R., Simpson R.J.;
 RT "Purification and NH2-terminal amino acid sequence of a
 RT T-cell-derived lymphokine with growth factor activity for B-cell
 RT hybridomas.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:9679-9683(1986).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 DR EMBL: X06203; CAA29560.1; -
 DR EMBL: M20572; AAA39302.1; -
 DR EMBL: X51457; CAA35824.1; -
 DR EMBL: J03783; AAA39301.1; -
 DR EMBL: X54542; CAA38412; -
 DR EMBL: M24221; AAA68814.1; -
 DR PIR: A30531; ICMS6.
 DR HSP: P05231; IALU.
 DR MGD: MGI:96539; IL6.
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6; 1.
 DR Cytokine; Growth factor; Glycoprotein; Signal.
 KW SIGNAL
 FT CHAIN 1 24
 FT CHAIN 25 211 INTERLEUKIN-6.
 FT DISULFID 70 76 BY SIMILARITY.
 FT DISULFID 99 109 BY SIMILARITY.
 SQ SEQUENCE 211 AA: 24384 MW: 88470DA9E86787A CRC64;

Query Match 100.0%; Score 1098; DB 1; Length 211;
 Best Local Similarity 100.0%; Pred. No. 6.8e-84;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFLSARDHPVAFGLMLVTTAFTSOVRKDFEDTTPNRPVYTSQVGLITHVLM 60
 DB 1 MKFLSARDHPVAFGLMLVTTAFTSOVRKDFEDTTPNRPVYTSQVGLITHVLM 60
 QY 61 EYEMKELCNGSDCMNDDALAENNLKLPETQRNDGCGYGTGNOEICLKISSLLEY 120

DB 61 EYEMKELCNGSDCMNDDALAENNLKLPETQRNDGCGYGTGNOEICLKISSLLEY 120
 QY 121 HSYLEVMKNNLKDNKKDKARVLQRPETLHIFNOVKDLHIVLPTPSNALLTDKLES 180
 DB 121 HSYLEVMKNNLKDNKKDKARVLQRPETLHIFNOVKDLHIVLPTPSNALLTDKLES 180
 QY 181 OKEMLRKTQIPLKSLSEEFKLVTLRSTROT 211
 DB 181 OKEMLRKTQIPLKSLSEEFKLVTLRSTROT 211

RESULT 2
 IL6_RAT
 ID IL6_RAT STANDARD; PRT: 211 AA.
 AC P20607;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-6 PRECURSOR (IL-6).
 GN IL6 OR IL-6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89380206; PubMed-2789217;
 RA Norhemann W., Braciak T.A., Hattori M., Lee F., Fey G.H.;
 RT "Structure of the rat interleukin 6 gene and its expression in
 RT macrophage-derived cells.";
 RL J. Biol. Chem. 264:16072-16082(1989).
 CC -1- FUNCTION: IL6 IS A CYTOKINE WITH A WIDE VARIETY OF BIOLOGICAL
 CC OF B-CELLS INTO IG-SECRETING CELLS, IT INDUCES MYELOMA AND
 CC PLASMACYTOMA GROWTH, IT INDUCES NERVE CELLS DIFFERENTIATION, IN
 CC HEPATOCYTES IT INDUCES ACUTE PHASE REACTANTS.
 CC -1- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
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 CC -----
 DR EMBL: M26744; AAA77659.1; -
 DR EMBL: M26745; AAA1430.1; -
 DR PIR: A34247; A34247.
 DR HSP: P05231; IALU.
 DR InterPro: IPR001716; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6CSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6; 1.
 DR Cytokine; Growth factor; Glycoprotein; Signal.
 KW SIGNAL
 FT CHAIN 1 24
 FT CHAIN 25 211 INTERLEUKIN-6.
 FT DISULFID 70 76 BY SIMILARITY.
 FT DISULFID 99 109 BY SIMILARITY.
 SQ SEQUENCE 211 AA: 24357 MW: 170248A14F96B5C1 CRC64;

Query Match 86.0%; Score 944; DB 1; Length 211;
 Best Local Similarity 85.3%; Pred. No. 3.5e-71;
 Matches 180; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MKFLSARDHPVAFGLMLVTTAFTSOVRKDFEDTTPNRPVYTSQVGLITHVLM 60
 DB 1 MKFLSARDHPVAFGLMLVTTAFTSOVRKDFEDTTPNRPVYTSQVGLITHVLM 60
 QY 61 EYEMKELCNGSDCMNDDALAENNLKLPETQRNDGCGYGTGNOEICLKISSLLEY 120

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OM protein - protein search, using sw model

Run on: October 4, 2001, 19:12:34 ; Search time 27.34 Seconds

(without alignments)
264.371 Million cell updates/sec

Title: us-09-230-048-4

Perfect score: 1098

Sequence: 1 MKPLSARDFHVAFLGLMLV.....FILKSLPEFLKVLTRSTRÖT 211

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1098	100.0	211	IL6_MOUSE	P08505 mus musculus
2	944	86.0	211	IL6_RAT	P20607 rattus norv
3	475	43.3	207	IL6_MAMO	O35736 maromota mon
4	428.5	39.0	212	IL6_PIG	P26893 sus scrofa
5	424.5	38.7	208	IL6_CAPII	O28319 capra hircu
6	422.5	38.5	208	IL6_BOVIN	P26892 bos taurus
7	420.5	38.3	208	IL6_HORSE	O95181 equus caball
8	420.5	38.3	212	IL6_HUMAN	P05231 homo sapien
9	419.5	38.2	205	IL6_ORCOR	O28747 orclunus orc
10	419.5	38.2	208	IL6_SHEEP	P29455 ovis aries
11	415.5	37.8	212	IL6_MACFA	P79341 macaca fasc
12	414.5	37.8	212	IL6_CERTO	P46550 cercopithec
13	413.5	37.7	209	IL6_PHOVI	O28819 phoca vitul
14	411.5	37.5	212	IL6_MACMU	P51594 macaca mula
15	401.5	36.6	208	IL6_FELCA	P41683 felis silve
16	386	35.2	207	IL6_CANFA	P41323 canis fami
17	229.5	20.9	125	IL6_MOUSE	P41593 mustela vis
18	95	8.5	201	IL6_CHICK	P13854 gallus gall
19	93.5	8.5	534	IL6_MOUSE	O03764 saccharomyc
20	92.5	8.4	261	IL6_MOUSE	P77339 escherichia
21	91.5	8.3	263	IL6_MOUSE	O02224 homo sapien
22	84.5	7.7	128	IL6_MOUSE	O13201 homo sapien
23	83.5	7.6	128	IL6_MOUSE	O73673 paracitellus
24	83	7.6	1170	IL6_MOUSE	P38989 saccharomyc
25	82.5	7.5	911	IL6_MOUSE	O94900 rattus norv
26	82	7.5	720	IL6_MOUSE	O59638 schizosacch
27	82	7.5	750	IL6_MOUSE	P49643 oncorhynch
28	81.5	7.4	326	IL6_MOUSE	P40531 saccharomyc
29	81	7.4	176	IL6_MOUSE	P26895 bos taurus
30	81	7.4	443	IL6_MOUSE	P07277 saccharomyc
31	81	7.4	559	IL6_MOUSE	O91637 xenopus lae
32	81	7.4	1064	IL6_MOUSE	O60307 methanococ
33	80.5	7.3	756	IL6_MOUSE	O49419 mycoplasma

34	80.5	7.3	1111	1	KIP1_YEAST	P28742 saccharomyc
35	80	7.3	377	1	TDP_DROME	O24318 drosophila
36	80	7.3	525	1	ASF2_YEAST	P32448 saccharomyc
37	80	7.3	584	1	CNA1_DROME	P12252 drosophila
38	80	7.3	623	1	RPOC_GUTTH	O78484 guillardi
39	80	7.3	954	1	DRP2_HUMAN	O13474 homo sapien
40	79.5	7.2	555	1	YNS2_YEAST	P53877 saccharomyc
41	79	7.2	176	1	IL7_SHEEP	O28540 ovis aries
42	79	7.2	1038	1	DPOD_CANAL	P46588 candida alb
43	78.5	7.1	425	1	YBYO_YEAST	P38272 saccharomyc
44	78.5	7.1	454	1	DNA_HAEIN	P43742 haemophilus
45	78.5	7.1	515	1	TRPE_BUCAP	P42387 buchiera ap

ALIGNMENTS

RESULT	ID	IL6_MOUSE	STANDARD	PRT	211 AA
AC	P08505	IL6_MOUSE	STANDARD	PRT	211 AA
DT	01-AUG-1988 (Rel. 08, Created)				
DT	01-AUG-1988 (Rel. 08, Last sequence update)				
DT	15-JUL-1998 (Rel. 36, Last annotation update)				
DE	INTERLEUKIN-6 PRECURSOR (IL-6) (INTERLEUKIN HP-1) (B-CELL HYBRIDOMA GROWTH FACTOR).				
DE	IL6 OR IL-6.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_Taxid=10090;				
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE=8166883; PubMed=2965020;				
RA	van Snick J., Cayphas S., Szikora J.-P., Renaud J.-C., van Roost E.,				
RA	Boon T., Simpson R.J.;				
RT	cDNA cloning of murine Interleukin-HP1: homology with human				
RT	Interleukin 6.;				
RL	Eur. J. Immunol. 18:193-197(1988).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=8903525; PubMed=3263439;				
RA	Tanabe O., Akira S., Kamiya T., Wong G.-G., Hirano T., Kishimoto T.;				
RT	Genomic structure of the murine IL-6 gene. High degree conservation				
RT	of potential regulatory sequences between mouse and human.;				
RL	J. Immunol. 141:3875-3881(1988).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=BAIB/C;				
RX	MEDLINE=91057159; PubMed=2243807;				
RA	Grenett H.E., Fuentes N.L., Fuller G.M.;				
RT	*Cloning and sequence analysis of the cDNA for murine Interleukin-6.;				
RL	Nucleic Acids Res. 18:6455-6455(1990).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=89017145; PubMed=3262872;				
RA	Chiu C.-P., Moulds C., Coffman R.L., Rennick D., Lee F.;				
RT	*Multiple biological activities are expressed by a mouse Interleukin				
RT	6 cDNA clone isolated from bone marrow stromal cells.;				
RL	Proc. Natl. Acad. Sci. U.S.A. 85:7099-7103(1988).				
RN	[5]				
RP	SEQUENCE OF 5-211 FROM N.A.				
RC	STRAIN=C57BL/6J;				
RX	MEDLINE=89124383; PubMed=2563387;				
RA	Mock B.A., Nordan R.P., Justice M.J., Kozak C., Jenkins N.A.;				
RT	*The murine IL-6 gene maps to the proximal region of chromosome 5.;				
RL	J. Immunol. 142:1372-1376(1989).				
RN	[6]				
RP	SEQUENCE OF 1-6 FROM N.A.				
RC	STRAIN=BAIB/C;				
RX	MEDLINE=90171860; PubMed=2106569;				
RA	Blankenstein T., Qin Z., Li W., Diamantstein T.;				

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 17:36:04 ; Search time 38.09 Seconds

(without alignments)
3041.701 Million cell updates/sec

Title: US-09-230-048-1

Perfect score: 612
Sequence: 1 ATCTGCTGCTCAAGTTGTC.....CTCCTGACGTCACGATAC 612

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*

1: /cgn2_6/ptodata/2/1na/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/1na/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/1na/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/1na/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/1na/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/1na/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	612	100.0	615	2	US-08-748-640-1
2	612	100.0	615	2	US-08-686-349-1
3	612	100.0	35100	2	US-08-770-379-17
4	612	100.0	35100	4	US-08-757-669A-17
5	61	10.0	555	2	US-08-945-529-7
6	54.6	8.9	555	1	US-08-567-047-1
7	54.6	8.9	555	2	US-08-693-182-1
8	54.6	8.9	555	2	US-08-567-048-1
9	54.6	8.9	555	2	US-09-008-482-1
10	53.6	8.8	564	1	US-07-918-181A-3
11	53.6	8.8	564	1	US-07-918-181A-7
12	53.6	8.8	564	1	US-08-231-575-3
13	53.6	8.8	564	1	US-08-231-575-7
14	53.6	8.8	564	1	PCT-US93-06928-3
15	53.6	8.8	564	5	PCT-US93-06928-7
16	53	8.7	555	2	US-08-009-973-2
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18	53	8.7	555	2	US-08-945-529-4
19	53	8.7	555	2	US-08-945-529-5
20	53	8.7	555	2	US-08-945-529-6
21	53	8.7	561	1	US-07-745-382-19
22	53	8.7	561	1	US-07-921-848-19
23	53	8.7	561	1	US-08-165-301A-19
24	53	8.7	561	3	US-08-810-436-19
25	52	8.5	564	1	PCT-US94-14179-19
26	52	8.5	564	1	US-07-918-181A-1
27	52	8.5	564	1	US-07-918-181A-5

28	52	8.5	564	1	US-08-231-575-1	Sequence 1, Appl
29	52	8.5	564	1	US-08-231-575-5	Sequence 5, Appl
30	52	8.5	564	5	PCT-US93-06928-1	Sequence 1, Appl
31	52	8.5	564	5	PCT-US93-06928-5	Sequence 5, Appl
32	51.4	8.4	540	4	US-08-149-101A-3	Sequence 3, Appl
33	51.4	8.4	540	5	PCT-US94-12873-3	Sequence 3, Appl
34	51.4	8.4	555	1	US-08-437-680A-1	Sequence 1, Appl
35	51.4	8.4	561	3	US-08-469-318-175	Sequence 175, App
36	51.4	8.4	561	3	US-08-468-609A-175	Sequence 175, App
37	51.4	8.4	561	5	PCT-US95-01185-175	Sequence 175, App
38	51.4	8.4	951	3	US-08-468-318-57	Sequence 57, Appl
39	51.4	8.4	951	3	US-08-468-609A-57	Sequence 57, Appl
40	51.4	8.4	951	5	PCT-US95-01185-57	Sequence 57, Appl
41	51.4	8.4	1128	4	US-08-795-473B-1	Sequence 1, Appl
42	51.4	8.4	1145	6	5510472-1	Patent No. 5510472
43	49.6	8.1	564	5	PCT-US92-05612-1	Sequence 1, Appl
44	49.6	8.1	564	5	PCT-US94-04208-6	Sequence 6, Appl
45	49.6	8.1	566	1	US-08-209-182C-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-748-640-1
; Sequence 1, Application US/08748640
; Patent No. 5854398
GENERAL INFORMATION:
APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: KAPOSI'S SARCOMA-ASSOCIATED HERPES VIRUS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,640
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 51731-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..615
US-08-748-640-1

Db 601 GTCCACGATAG 612

RESULT 3

US-08-770-379-17/c

Sequence 17, Application US/08770379

Patent No. 5849564

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Edelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: POLYPEPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED

TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/770.379

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 52342

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 35100 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-770-379-17

Query Match 100.0%; Score 612; DB 2; Length 35100;

Best Local Similarity 100.0%; Pred. No. 2.5e-200;

Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCTGCTGCTCAAGTGTGCTCTCTGTCGCTGCTCACTGCTGCTATCTGGAACG 60
DB 17875 ATGCTGCTGCTCAAGTGTGCTCTCTGTCGCTGCTCACTGCTGCTATCTGGAACG 17816
QY 61 CGGGGCAAGTTCGCGAGCCCGCCGAGTTGAAAGGATCTCTCATTTAGAGACTGCAT 120
DB 17815 CGGGGCAAGTTCGCGAGCCCGCCGAGTTGAAAGGATCTCTCATTTAGAGACTGCAT 17756
QY 121 TGGATGCTATGCGTATGCTGATGCTTCCGCGACTCTGTTACGCTACCGGATCTGC 180
DB 17755 TGGATGCTATGCGTATGCTGATGCTTCCGCGACTCTGTTACGCTACCGGATCTGC 17696
QY 181 AAGGCTATTTCTAGAGCCGCTCTATTTTTCATCTGAAACTACCAAGCTCAACGATCT 240
DB 17695 AAGGCTATTTCTAGAGCCGCTCTATTTTTCATCTGAAACTACCAAGCTCAACGATCT 17636
QY 241 GATCACTGCGGGTAAATAGATTTAATGAGACTAGCTGCTTAAAAAGCTCGCGGATGCG 300
DB 17635 GATCACTGCGGGTAAATAGATTTAATGAGACTAGCTGCTTAAAAAGCTCGCGGATGCG 17576

QY 301 TTTTGTGAATTCGAGGTGTTGTTTAAAGTTTAAACGAGGATTTGSAATTCAGTGATA 360
DB 17575 TTTTGTGAATTCGAGGTGTTGTTTAAAGTTTAAACGAGGATTTGSAATTCAGTGATA 17516
QY 361 AACGTGAGCTGATGAGCTTCTGACGAAGACCTTAGATGAGATACAGGAAGAGCTC 420
DB 17515 AACGTGAGCTGATGAGCTTCTGACGAAGACCTTAGATGAGATACAGGAAGAGCTC 17456
QY 421 AATAAGCTGACTAAGACGACATACAGTCCACCAATTTGACCGGGCTTATTAGGAGC 480
DB 17455 AATAAGCTGACTAAGACGACATACAGTCCACCAATTTGACCGGGCTTATTAGGAGC 17396
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DB 17395 CTTGAGGACCTTAAGATATGAGTGAACACTTGTCTGTTTATGTTCTGATGCAATG 17336
QY 541 GAAAGTTTGCAGGTCAACGCGGTGCTTTTGGACTATATCCAGACGTGACTCTGCAC 600
DB 17335 GAAAGTTTGCAGGTCAACGCGGTGCTTTTGGACTATATCCAGACGTGACTCTGCAC 17276
QY 601 GTCCACGATAG 612
DB 17275 GTCCACGATAG 17264

RESULT 4

US-08-757-669A-17/c

Sequence 17, Application US/08757669A

Patent No. 6183751

GENERAL INFORMATION:

APPLICANT: Chang, Yuan

APPLICANT: Bohenzky, Roy A.

APPLICANT: Russo, James J.

APPLICANT: Edelman, Isidore S.

APPLICANT: Moore, Patrick S.

TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS

TITLE OF INVENTION: SEQUENCES AND USES THEREOF

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper & Dunham LLP

STREET: 1185 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/757.669A

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: White, John P.

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 45185-F

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 278-0400

TELEFAX: (212) 391-0525

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 35100 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-757-669A-17

Query Match 100.0%; Score 612; DB 4; Length 35100;

ADDRESS: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/567,047
FILING DATE: 04-DEC-1995
CLASSIFICATION: 530
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/387,924
FILING DATE: 23-FEB-1995
APPLICATION NUMBER: IT RM93A000409
FILING DATE: 23-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: SAVINO-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ANTI-SENSE: no
FRAGMENT TYPE: internal
IMMEDIATE SOURCE:
LIBRARY: production in bacteria
FEATURE:
NAME/KEY: IL-6 cDNA
IDENTIFICATION METHOD: polyacrylamide gel
NAME/KEY: CDS
LOCATION: 1..552
US-08-567-047-1

Query Match 8.9%; Score 54.6; DB 1; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 160 TGTTCACGACGCGATCGCAAGGATATCTAGAGCCGCGCTATTTTTCATCGAAA 219
DB 130 TGTAAACAAGATGATGTTGAAGCAGCAAGGCGCATGCGCAAAAAACAACCTGAAC 189
QY 220 CTACAGCCATCAAGATGATGATCACTGCGGTTAATAGATTAAAGATGATGATGCTG 279
DB 190 CTTCGAAGATGCTGCAAAAGATGATGATGATGATGATGATGATGATGATGATGATG 249
QY 280 CTTAAAAAGCTGCGGAGCGCTTTTGTGAATTCGAGCTGTTGTGAATTTTAAACGACG 339
DB 250 CTGTTGAATTAATCATCATCTGTTTGTGAGTTTGAAGTATACCTAGAGTACCTCCGAAAC 309
QY 340 GAGTTTGAATTAATCATCATCTGTTTGTGAGTTTGAAGTATACCTAGAGTACCTCCGAAAC 399
DB 310 ACATTTGACAGTAGTAGAGCAACGCGATGCTGCTCAGATAGTACCAAAAGTCTGATC 369
QY 400 TGGGACATACAGAGAGCTCAATAGCTAGTACAGACATACAGTACAGTACAGTACAGTAC 459
DB 370 CAGTTCTCTCAAAAAAGCAAAAGATCTAGATGCAATAGCAACCCCTGACCAACACACA 429
QY 460 GACCCGCGTCTATTAGGAGGCTTACAGGACCTTAAGTATTGGGTGAGACACTTTGCTTGC 519

DB 430 AATGCCACCTGCTGACGACGCTGACGACGACGACGACGACGACGACGACGACGACGAC 489
QY 520 TTTATGTTGAGTGCATGCAATGCAAAAGTT 548
DB 490 CATCTCATCTGATCTTTTAAGAGATT 518

RESULT 7
US-08-693-182-1
Sequence 1, Application US/08693182
Patent No. 5849283
GENERAL INFORMATION:
APPLICANT: CILIBERTO, Gennaro
APPLICANT: SAVINO, Rocco
APPLICANT: LAHN, Armin
APPLICANT: TONINATTI, Carlo
TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
TITLE OF INVENTION: SUPERAGONISTS, ANTAGONISTS AND SUPERANTAGONISTS OF HUMAN
TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: Browdy and Neimark, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
COUNTRY: United States of America
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,182
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/IT95/00216
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IT RM 94A000805
FILING DATE: 14-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: CILIBERTO-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 555 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..552
US-08-693-182-1

Query Match 8.9%; Score 54.6; DB 2; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

QY 160 TGTTCACGACGCGATCGCAAGGATATCTAGAGCCGCGCTATTTTTCATCGAAA 219
DB 130 TGTAAACAAGATGATGTTGAAGCAGCAAGGCGCATGCGCAAAAAACAACCTGAAC 189
QY 220 CTACAGCCATCAAGATGATGATCACTGCGGTTAATAGATTAAAGATGATGATGCTG 279

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Db 190 CTTTCAAGATGCGTGAAGAAAGATGATGCTTCCAAATCTGGATTCATGAGAGACTTGC 249
QY 280 CTTTAAAGCTCGCCGATGCTTTTGAATTCGAGGTGTTGTTTAAAGTTTAAACGACG 339
Db 250 CTTGCTGAAGATCATCACTGCGCTTTTGGAGTTTACGATATACCTAGACTACTCCAGAAC 309
QY 340 GAGTTTGAAGAAATCAGTATTAACCTGAGCTCATGAGCTTCTGACCAAGACTTGA 399
Db 310 AGATTGAGTAGTAGAGAGTCAAGCCAGAGCTGTCAGATGAGTCAAGAAAGTCTGATC 369
QY 400 TGGACATATACAGAGAGCTCAATTAAGCTGACTTAAGACGACTACCTGACCCCAATTT 459
Db 370 CAGTTCTCGCAAGAAAGCCAAAGATCTAGATCAATTAACCCCTGACCCAGACACA 429
QY 460 GACCGCGCTATTAAGGAGGCTTGAGGACTTAAGTATTTGGGTGAGACACTTTGCTTG 519
Db 430 AATGCCAGCCTGCTGAGCAAGCTGACGACAGCAAGCAGTGGCTGACGAGCATACACT 489
QY 520 TTTTATCTTCTGAGTCAATGCAAAAGTT 548
Db 490 CATCTCATCTGAGATCTTTAAGAGTT 518

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RESULT 8

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US-08-567-048-1
; Sequence 1, Application US/08567048
; Patent No. 5891998
; GENERAL INFORMATION:
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: CILIBERTO, Gennaro
; TITLE OF INVENTION: METHOD FOR SELECTING SUPRAGONISTS,
; TITLE OF INVENTION: ANTAGONISTS AND SUPRAGONISTS FOR HORMONES HAVING
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESS: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/567,048
; FILING DATE: 04-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,924
; FILING DATE: 23-FEB-1995
; APPLICATION NUMBER: IT RM93A000409
; FILING DATE: 23-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SAVINO-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ANTI-SENSE: no

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; FRAGMENT TYPE: Internal
; IMMEDIATE SOURCE:
; LIBRARY: production in bacteria
; FEATURE:
; NAME/KEY: IL-6 cDNA
; IDENTIFICATION METHOD: polyacrylamide gel
; NAME/KEY: CDS
; LOCATION: 1..552
; US-08-567-048-1

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Query Match 8.98; Score 54.6; DB 2; Length 555;
 Best Local Similarity 46.34; Pred. No. 3.7e-09;
 Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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QY 160 TGTACCGTACCGCATCTGCAAGGATTTCTAGAGCCGCTGATTTTTCATCTGAAA 219
Db 130 TGTACCAAGAGTAACTAGTGTGAAAGACGCAAGAGGACTGCGCAAAACACCTGAAAC 189
QY 220 CTACAGCATCAAGATGATGATGATGCGGTTAATGAGATTAAATGAGACTAGCTGC 279
Db 190 CTTCAAGAGATGCTGAAAAAGATGATGATGATGATGATGATGATGATGATGATGATG 249
QY 280 CTTTAAAGCTCGCCGATGCTTTTGAATTCGAGGTGTTTAAAGTTTAAACGACG 339
Db 250 CTTGCTGAAGATCATCACTGCGCTTTTGGAGTTTACGATGATGATGATGATGATGATG 309
QY 340 GAGTTTGAAGAAATCAGTATTAACCTGAGCTCATGAGCTTCTGACCAAGACTTGA 399
Db 310 AGATTGAGTAGTAGAGAGTCAAGCCAGAGCTGTCAGATGAGTCAAGAAAGTCTGATC 369
QY 400 TGGACATATACAGAGAGCTCAATTAAGCTGACTTAAGACGACTACCTGACCCCAATTT 459
Db 370 CAGTTCTCGCAAGAAAGCCAAAGATCTAGATCAATTAACCCCTGACCCAGACACA 429
QY 460 GACCGCGCTATTAAGGAGGCTTGAGGACTTAAGTATTTGGGTGAGACACTTTGCTTG 519
Db 430 AATGCCAGCCTGCTGAGCAAGCTGACGACAGCAAGCAGTGGCTGACGAGCATACACT 489
QY 520 TTTTATCTTCTGAGTCAATGCAAAAGTT 548
Db 490 CATCTCATCTGAGATCTTTAAGAGTT 518

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RESULT 9

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US-09-008-482-1
; Sequence 1, Application US/09008482
; Patent No. 5914106
; GENERAL INFORMATION:
; APPLICANT: CILIBERTO, Gennaro
; APPLICANT: SAVINO, Rocco
; APPLICANT: LAHM, Armin
; APPLICANT: TONIAPI, Carlo
; TITLE OF INVENTION: A METHODOLOGY FOR SELECTING
; TITLE OF INVENTION: SUPRAGONISTS, ANTAGONISTS AND SUPRAGONISTS OF HUMAN
; TITLE OF INVENTION: INTERLEUKIN-6 BASED ON RECEPTOR COMPLEX THREE DIMENSIONAL
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESS: Browdy and Neimark, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/008,482

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: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: USSN 08/693,182
: FILING DATE: 14-AUG-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/IT95/00216
: FILING DATE: 13-DEC-1995
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: IT RM 94A000805
: FILING DATE: 14-DEC-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: YUN, Allen C.
: REGISTRATION NUMBER: 37,971
: REFERENCE/DOCKET NUMBER: CILIBERTO-2A
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 555 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..552
: US-09-008-482-1

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Query Match      8.9%; Score 54.6; DB 2; Length 555;
Best Local Similarity 46.3%; Pred. No. 3.7e-09;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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QY 160 TGTATACCGTACCGGCTTCGCAAGGCTATTCTAGAGCCCGCTCTTTTTCATCTGAAA 219
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DB 130 TGTAAACAGAGTAACTGTTGTGAAGACACCAAGAGGCACTGCGACAGAAAACACCTGAA 189
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 220 CTACACGACCATCAACGATCTGATCACTGCGGGTAAATAGATTATAGAGTACTGTC 279
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 190 CTTCCAAAGATGCTTAAGAAAGATGATGCTTCCATCTGATTCATGAGGAGACTTGC 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 280 CTTAAAGACGCGCGGCTTTTGAATTCGAGGTGTTGTTAAAGTTTAAAGAGC 339
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 250 CTGCGTAAATATCACTGCTGTTTGGAGTTTGAAGTAACTAGAGTACCTCCAGAAC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 340 GACTTTGGAATACATGATTAACGTCGACGTCATGAGCTTCTGACGAAGACCTTAGCA 399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 310 AGATTGGAAGTAGTAGAGTCAAGCCAGAGCTGTCCAGATGAGTCAAAAGTCTGATC 369
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 400 TGGACATACAGGAAGGCTCAATTAAGCTGACTAAGACGACGACTACACCAAAATTT 459
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 370 CAGTTCTCTGAGAAAAGGCAAAAGATTAAGATGCAATTAACACCCCTGACCCACACA 429
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QY 460 GACCGCGGTCTATTAGGAGGCTTCAGAGGACTTAAGTATTGGGTGAGACACTTGGTTCG 519
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DB 430 AATGCCAGCGCTGTCGACGAAGCTGCAAGGCAAGACCAACGAGCTGCGAGGACATGAC 489
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QY 520 TTTTATGTTCTGAGTCAATGCAAAAGTT 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 490 CATCTCATCTTGAGATCTTTTAAGGAGTT 518
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: RESULT 10
: US-07-918-181A-3
: Sequence 3, Application US/07918181A
: Patent No. 533833
: GENERAL INFORMATION:
: APPLICANT: Fowlkes, Dana M.
: TITLE OF INVENTION: C-Terminal IL-6 Mutelins
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Imclone Systems Incorporated

```

```

: STREET: 180 Varick Street
: CITY: New York
: STATE: New York
: COUNTRY: United States
: ZIP: 10014
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/07/918,181A
: FILING DATE: 23-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Sheets, Eric J.
: REGISTRATION NUMBER: 30,326
: REFERENCE/DOCKET NUMBER: FOW-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212-645-1405
: TELEFAX: 212-645-2054
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 564 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..558
: NAME/KEY: mat_peptide
: LOCATION: 1..555
: US-07-918-181A-3

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Query Match      8.8%; Score 53.6; DB 1; Length 564;
Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

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QY 154 GACCTCTGTACCGTACCGGCTATGCAAGGTATTCTAGAGCCCGCTGATTTTTCAT 213
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DB 127 GAACTCTGTAAAGAGTAACTATGTTGAAAGCAGTAAAGAACACTGCGAGAAAACAC 186
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 214 CTGAACCTACCAAGCATCAAGATGATCACTGCGGGTAAATAGATTAAAGAGACT 273
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 187 CTGAACCTCCGAAGATGCTGAAAAGATGATGATTTTCAATCTGATTCATGAGGAA 246
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 274 AGCTGCTTAAAGAGCTCGCGGATGCTTTTGAATTCGAGGTGTTTAAAGTTTAA 333
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 247 ACTTGTCTGTGAATAATCATACAGCGCTTTTGAATTGAGGTATTAACCTAGAGTACT 306
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 334 ACAGAGAGTTTGAAGAAATCAGTATTAAGCTGAGCTCATGGAGCTTTCAGAGAAAGC 393
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 307 CAGAACAGATTTTGAAGTATGAGTATGAGAACAGAGAGCTTCCAGATGTCGACCAAGTC 366
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 394 TTAGATGAGACATACAGGAAGAGCTCAATTAAGCTGATTAAGAGCAGTACAGTCCACC 453
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DB 367 CTGATCCAGTTTCTGCAGAAAAGGCAAAAATCTAGATGCAATTAACACCCCGGATCCA 426
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 454 AAATTTGACCGCGGTCTATTAGGAGGCTTCAGGAGCTTAAGTATGGCTGAGACACTTT 513
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 427 ACCAACAATGCGAGCTGTCGACGAGCTGACAGGACAGACAGACGAGGCTGAGAGATG 486
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QY 514 GCTTCGTTTATGTTCTGAGTGAATGGAAGATTTCAGAGTCAAGCGGTGCGCTGTTTG 573
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 487 ACAATCATCTATCTTGAGATCTTTGAAAGAAATCTCTGAGAGTCTCCGCTGCTCTG 546
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: RESULT 11

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Db 247 ACTTGCTGGTGAATAATCATATCAGAGCCCTTTGGAAATTTGAGATATACCTAGAGTACCTC 306
OY 334 ACCAGCAGCTTTGGAATAATCATATGATAACGTGACCTCATGAGCTTGTGACGAGACCC 393
Db 307 CAGAACAGATTGAGAGTGTAGTGAGAACAGCAGAGCTGTCCAGTATGTGACCAAAAGTC 366
OY 394 TTAGATGGGACATACAGAGAGAGCTCAATTAAGCTGACTAAGACGCACTACAGTCCACC 453
Db 367 CTGATCCAGTTTCTGCAAGAAAAGCAAAATCTAGATGCAATTAACCAACCCCGATCCA 426
OY 454 AAATTGACCGGGGTCTATTAGGAGAGCTTCAGAGCTTAAGTATTGGGTGAGACACTT 513
Db 427 ACCACAAATGCGAGCTGTGACGAGCTGACAGCAGACCAAGTGGCTGACGAGACATG 486
OY 514 GCTTCGTTTATGTCGTGAGTGCATGAAAGTTTGACAGTCAACGGGCTGCTTTTG 573
Db 487 ACAACTCATCTCATTTCTGAGATCTTTGAAAGAAATTCCTGACAGTCTCCCTGCTGCTG 546

RESULT 13

US-08-231-575-7
Sequence 7, Application US/08231575

Patent No. 5565336
GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: C-Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,575
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Sheets, Eric J.
REGISTRATION NUMBER: 30,326
REFERENCE/DOCKET NUMBER: FOW-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: NO
NAME/KEY: CDS
LOCATION: 1..558
NAME/KEY: mat_peptide
LOCATION: 1..555
US-08-231-575-7

Query Match 8.8%; Score 53.6; DB 1; Length 564;

Best Local Similarity 45.5%; Pred. No. 8.4e-09;
Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

OY 154 GACCTCTGTATACCGTCCCGCATCTGCAAGGGATATTCFAGAGGCCCTCTATTTTCAT 213
Db 127 GAGACCTGTATACAGATGATACATGTGTGAAGCAGTAAAGACACTGTCAGAAAACAC 186
OY 214 CTGAACATCAAGCCATCAAGATACATGATCACTGCGGGTTAATAGATTATAGAGCT 273
Db 187 CTGAACCTTCCGAAGATGGCTGAAAAGATGATGATTTCATCTGATTCATTAAGGAA 246
OY 274 AGCTGCTTAAAGACTCCCGCATGCTTTTGAATGAGAGTGTGTTAAGTTTAA 333
Db 247 ACTTGCTGGTGAATAATCATATCAGAGCCCTTTGGAATTTGAGTATACCTAGAGTACCTC 306
OY 334 ACCAGCAGCTTTGGAATAATCATAGTATAACGTGACCTCATGAGCTTGTGACGAGACCC 393
Db 307 CAGAACAGATTGAGAGTGTAGTGAGAACAGCAGAGCTGTCCAGATGTGACCAAAAGTC 366
OY 394 TTAGATGGGACATACAGAGAGAGCTCAATTAAGCTGACTAAGACGCACTACAGTCCACC 453
Db 367 CTGATCCAGTTTCTGCAAGAAAAGCAAAATCTAGATGCAATTAACCAACCCCGATCCA 426
OY 454 AAATTGACCGGGGTCTATTAGGAGAGCTTCAGAGCTTAAGTATTGGGTGAGACACTT 513
Db 427 ACCACAAATGCGAGCTGTGACGAGCTGACAGCAGACCAAGTGGCTGACGAGACATG 486
OY 514 GCTTCGTTTATGTCGTGAGTGCATGAAAGTTTGACAGTCAACGGGCTGCTTTTG 573
Db 487 ACAACTCATCTCATTTCTGAGATCTTTGAAAGAAATTCATGACAGTCTCCCTGCTGCTG 546

RESULT 14

PCT-US93-06928-3

Sequence 3, Application PC/TUS9306928

GENERAL INFORMATION:
APPLICANT: Fowles, Dana M.
TITLE OF INVENTION: Carboxy Terminal IL-6 Mutelins
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
STREET: 180 Varick Street
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06928
FILING DATE: 19930723
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/918,181
FILING DATE: 23-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: FOW-2-T
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 564 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

Fri Oct . 5 10:02:05 2001

us-09-230-048-1.rni

Page 11

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:52:14 : Search time 74.43 Seconds
(Without alignments)
362.626 Million cell updates/sec

Title: US-09-230-048-2

Perfect score: 1095

Sequence: 1 MCMFKMLSLVGLVSGT.....GQAVVLDSDPPVDPVHK 204

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database :

Listing first 45 summaries

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SPREMBL_16:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	14	098823 Kaposi's sa
2	1093	99.8	204	14	040918 Kaposi's sa
3	182	16.6	209	6	09TTH3 actus lemur
4	179	16.3	209	6	097540 actus nancy
5	158	14.4	208	6	09XR80 delphinapte
6	154.5	14.1	207	6	09MY27 canis famli
7	143	13.1	175	6	09TTH4 actus nigril
8	138	12.6	207	11	09JTH3 marmota mon
9	136.5	12.5	207	6	028403 enhydra lut
10	132	12.1	160	6	097535 actus vocif
11	129.5	11.8	210	11	09WV08 mesocricetu
12	116.5	10.6	241	6	09MY27 oryctolagus
13	95	8.7	684	4	09UKR6 homo sapien
14	95	8.7	684	6	09TTH4 bos taurus
15	95	8.7	684	11	09QXK7 mus musculu
16	92.5	8.4	101	11	055041 cricetus
17	86.5	7.9	487	1	028450 archaeoglob
18	83.5	7.6	979	1	005477 sulfolobus
19	82.5	7.5	145	6	09WZ05 oryctolagus

20	82	7.5	367	14	041165 Parametium
21	81.5	7.4	442	5	09UC65 stylonychia
22	80.5	7.4	387	10	09LD24 chlorarachn
23	79.5	7.3	1030	3	09P18 plicha angu
24	79	7.2	385	5	009642 caenorhabd
25	78.5	7.2	387	10	09ZTQ1 chlorarachn
26	78.5	7.2	387	10	09SAL3 chlorarachn
27	78.5	7.2	674	5	090755 chlorarachn
28	78	7.1	118	6	09MK08 lepus callif
29	78	7.1	118	6	09MK07 lepus town
30	78	7.1	900	10	09PIU0 arabidopsis
31	77.5	7.1	333	14	065121 african swi
32	77	7.0	486	10	09L169 arabidops
33	77	7.0	1004	1	028412 archaeoglob
34	77	7.0	1810	10	09ZSD1 iactuca sat
35	76.5	7.0	461	3	094647 schizosacch
36	76	6.9	1005	2	09HRE6 pseudomonas
37	76	6.9	1849	5	09U487 loligo peal
38	75.5	6.9	164	5	044835 caenorhabd
39	75.5	6.9	236	5	09N4D9 caenorhabd
40	75.5	6.9	443	10	09LK18 thalassios
41	75.5	6.9	448	10	09STD0 zinnia eleg
42	75.5	6.9	602	2	09Z7J0 chlamydia p
43	75.5	6.9	1158	3	09UTR5 schizosacch
44	75	6.8	244	2	09WZ14 thermoga
45	75	6.8	524	5	077098 caenorhabd

ALIGNMENTS

RESULT 1
ID 098823 PRELIMINARY: PRT: 204 AA.

AC 098823; 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 HOMOLOG (FRAGMENT).
OS VIL-6.
OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_TaxID=37296;
RN [1]
RP SEQUENCE FROM N.A.
RA Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.J.,
RA Friedman-Kien A.E., Fleckenstein B.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Nicholas J., Ruvolo V.R., Burns W.H., Sandford G., Wan X., Clufo D.,
RA Hendrickson S., Guo H.G., Hayward G.S., Reitz M.S.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA MEDLINE-97094384; PubMed-8939871;
RX Moore P.S., Bashoff C., Weiss R.A., Chang Y.;
RT "Molecular mimicry of human cytokine and cytokine response pathway
RT genes by KSHV";
RL Science 274:1739-1744(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-97121480; PubMed-8962146;
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;
RT "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
RT (HHV8)";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
RN [5]
RP SEQUENCE FROM N.A.
RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena D.,
RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.;

RL Submitted (Oct-1996) to the EMBL/Genbank/DBJ databases.
 RN 161
 RP SEQUENCE FROM N.A.
 RA Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Magdalena D.,
 RA Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.,
 RL Submitted (Mar-1997) to the EMBL/Genbank/DBJ databases.
 RN 171
 RP SEQUENCE FROM N.A.
 RA Sun R., Lin S.-F., Miller G.,
 RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.
 DR EMBL: U73655; AAB18244.1; -
 DR EMBL: U67774; AAB61701.1; -
 DR EMBL: U75698; AAC57089.1; -
 DR EMBL: U71365; AAC34937.1; -
 DR InterPro: IPR003573; -
 DR Pfam: PF00489; IL6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 204
 FT SEQUENCE 204 AA; 23408 MW; 1CA7772A0EDC05EB CRC64;

Query Match 100.0%; Score 1095; DB 14; Length 204;
 Best Local Similarity 100.0%; Pred. No. 1.3e-99;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCFKMLSLVLSVSTGRKLPDAPFEKDLIQRLNMLWIDECFRDLCYRTGIC 60
 DB 1 MCFKMLSLVLSVSTGRKLPDAPFEKDLIQRLNMLWIDECFRDLCYRTGIC 60
 QY 61 KGLPEPAIFHLKLPAINDTDHGCLIGNETSCLKADGFEFEVLFKFLTTEGKSVI 120
 DB 61 KGLPEPAIFHLKLPAINDTDHGCLIGNETSCLKADGFEFEVLFKFLTTEGKSVI 120
 QY 121 NVDVVELLTKTGMDIOEELNKLTKTHYSPPKFDGDLGRLOGLKWVHFAFYLSAM 180
 DB 121 NVDVVELLTKTGMDIOEELNKLTKTHYSPPKFDGDLGRLOGLKWVHFAFYLSAM 180
 QY 181 EKFAQAVRVLDSIPDVPDVHDK 204
 DB 181 EKFAQAVRVLDSIPDVPDVHDK 204

RESULT 2
 ID 040918 PRELIMINARY: PRT; 204 AA.
 AC 040918;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE ORF K2, sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OS Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus 8).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae; Rhadinovirus.
 OX NCBI_Taxid=37296;
 RN 111
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97138401; PubMed-8985427;
 RA Neipel F., Albrecht J.C., Ensser A., Huang Y.Q., Li J.-J.,
 RA Friedman-Kien A.E., Fleckenstein B.,
 RT "Human herpesvirus 8 encodes a homolog of interleukin-6.";
 RL J. Virol. 71:839-842(1997).
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97296220; PubMed-9151804;
 RA Neipel F., Albrecht J.C., Fleckenstein B.,
 RT "Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus
 RT human herpesvirus 8: determinants of its pathogenicity?";
 RL J. Virol. 71:4187-4192(1997).
 DR EMBL: U93872; AAB62676.1; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR ProDom: PD004356; -; 1.

DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 204 AA; 23408 MW; 2F46737828AF20B9 CRC64;
 Query Match 99.8%; Score 1093; DB 14; Length 204;
 Best Local Similarity 99.5%; Pred. No. 2e-99;
 Matches 203; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCFKMLSLVLSVSTGRKLPDAPFEKDLIQRLNMLWIDECFRDLCYRTGIC 60
 DB 1 MCFKMLSLVLSVSTGRKLPDAPFEKDLIQRLNMLWIDECFRDLCYRTGIC 60
 QY 61 KGLPEPAIFHLKLPAINDTDHGCLIGNETSCLKADGFEFEVLFKFLTTEGKSVI 120
 DB 61 KGLPEPAIFHLKLPAINDTDHGCLIGNETSCLKADGFEFEVLFKFLTTEGKSVI 120
 QY 121 NVDVVELLTKTGMDIOEELNKLTKTHYSPPKFDGDLGRLOGLKWVHFAFYLSAM 180
 DB 121 NVDVVELLTKTGMDIOEELNKLTKTHYSPPKFDGDLGRLOGLKWVHFAFYLSAM 180
 QY 181 EKFAQAVRVLDSIPDVPDVHDK 204
 DB 181 EKFAQAVRVLDSIPDVPDVHDK 204

RESULT 3
 ID 09TH3 PRELIMINARY: PRT; 209 AA.
 AC 09TH3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Aotus lemurinus (Northern gray-necked night monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OX NCBI_Taxid=43147;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
 RA Patarroyo M.E.,
 RT "Aotus lemurinus gene for IL-6.";
 RL Submitted (Oct-1998) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF097323; AAF21290.1; -
 DR HSP: P05231; IAUU.
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFNGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 FT NON_TER 209
 FT SEQUENCE 209 AA; 23115 MW; A0A3DFAABF560CC CRC64;

Query Match 16.6%; Score 182; DB 6; Length 209;
 Best Local Similarity 26.5%; Pred. No. 4.5e-10;
 Matches 41; Conservative 36; Mismatches 78; Indels 0; Gaps 0;

QY 37 QRLNMLWIDECFRDLCYRTGICGILEPAIFHLKLPAINDTDHGCLIGNETSCLK 96
 DB 55 KIRIYLEISALRKICCKSNKESSEKALNNLIPKMAEKGCFCGSEETCLVK 114
 QY 97 LADGFEFEVLFKFLTTEGKSVINVDVVELLTKTGMDIOEELNKLTKTHYSPPKFDG 156
 DB 115 ITTGLLEFEYLEYLONKRESSKEAGAVQSTKGLISQKKAKNLSAIPDPATNS 174
 QY 157 LIGRLOGLKWVHFAFYLSAMEKFAQAVRV 191
 DB 175 LLMKIQADQWQGVYTHLILRSFKELQSLRAL 209


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RESULT 4
097540 ID 097540 PRELIMINARY; PRT; 209 AA.
AC 097540;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6 (FRAGMENT).
GN IL-6.
OS Aotus nancymae (Owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN 11
RP SEQUENCE FROM N.A.
RA Echeverry S.J., Hernandez E., Moreno A., Patatroyo M.E., Murillo L.A.;
RT "Identification, cloning and sequencing of different interleukin genes
RT in 4 Aotus species.";
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF014510; AAD01536.1;
DR HSSP: P05231; IAUU
DR InterPro: IPR003573;
DR InterPro: IPR003574;
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6CSFMGE.
DR PRINTS: PS00254; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
FT NON_TER 1
FT NON_TER 209
SQ SEQUENCE 209 AA; 23406 MW; B84F085DD84002DD CRC64;

Query Match 16.3%; Score 179; DB 6; Length 209;
Best Local Similarity 26.5%; Pred. No. 8.9e-10;
Matches 41; Conservative 34; Mismatches 80; Indels 0; Gaps 0;

QY 37 ORLMMMLVVIDECFRDLCYRIGICGILPEPAIFHLKLPAINDRHCGLIGFNESCLCK 96
DB 55 KHIRILGICILARKETCNKSMCKSSKEALAEENLNLPKMAEKDCGSGNEETCLVK 114
QY 97 LADGFEFEVLFKFLTFTEFGKSVINVDVWELTKTGMDIOELNKLTKTHSPKPRDNG 156
DB 115 IITGLFEFVLEVLQNFESSEBQARAVOMSTKVLIOPLQKANKANDAITTPDTTAS 174
QY 157 ILGRLGLKYNVRHFASTFVLSAMEKFAQAVRVL 191
DB 175 LITKLAONOMLQDWTHTLIRSEKFEFLQSSLRAL 209

RESULT 5
09XT80 ID 09XT80 PRELIMINARY; PRT; 208 AA.
AC 09XT80;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN 6 PRECURSOR.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN 11
RP SEQUENCE FROM N.A.
RA St-Laurent G., De Guise S., Fournier M., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) interleukin 6.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF076643; AADA2929.1;
DR HSSP: P05231; IAUU.

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DR InterPro: IPR003573;
DR InterPro: IPR003574;
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6CSFMGE.
DR PRINTS: PRO0434; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
SQ SEQUENCE 208 AA; 23456 MW; 81CC85C6E80389C4 CRC64;

Query Match 14.4%; Score 158; DB 6; Length 208;
Best Local Similarity 22.3%; Pred. No. 1e-07;
Matches 44; Conservative 46; Mismatches 89; Indels 18; Gaps 4;

QY 12 VGSILVSGRGLKLPD--APEPEKDLILORL-----NMMLVVIDECFRDLCRT 57
DB 11 LGLLVYATAPPTPGPLAGDSDATNSLPLTSANKVEELIKYILGISAKRMCECY 70
QY 58 GICGILPEPAIFHLKLPAINDRHCGLIGFNESCLKADGFEFEVLFKFLTFTEFGK 117
DB 71 DKCENSKALAEENLNLPKMAEKDCGSGFNQETCLMRITTGLEYQIYLDYQNEVYG 130
QY 118 SYINVDVWELTKTGMDIOELNKLTKTHSPKPRDNGLGRLOGLK-YVVRHFASTFV 176
DB 131 DKGSIEAVQISIKALQILRKVRKNPDVTTTPDTTASLMMNLOSQDDMMRNTKIILI 190
QY 177 LSAME---KFAQAVRV 190
DB 191 LSTLENPLQFSLRVRI 207

RESULT 6
09MYZ7 ID 09MYZ7 PRELIMINARY; PRT; 207 AA.
AC 09MYZ7;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE INTERLEUKIN-6.
GN IL-6.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN 11
RP SEQUENCE FROM N.A.
RA Youn H.-Y., Shin I.-S.;
RT "Canine IL-6 mRNA.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF275796; AAF86275.1;
DR InterPro: IPR003573;
DR InterPro: IPR003574;
DR Pfam: PF00489; IL6; 1.
DR PRINTS: PRO0433; IL6CSFMGE.
DR PRINTS: PRO0434; INTERLEUKIN_6; 1.
DR PROSITE: PS00254; INTERLEUKIN_6; 1.
DR SMART: SM00126; IL6; 1.
SQ SEQUENCE 207 AA; 23042 MW; 45541AB011C80F50 CRC64;

Query Match 14.1%; Score 154.5; DB 6; Length 207;
Best Local Similarity 23.9%; Pred. No. 2.2e-07;
Matches 48; Conservative 38; Mismatches 98; Indels 17; Gaps 3;

QY 8 SLLVGSILVSGTRGKLP-----DA-----PEPEKDLILQRLNMMLVVIDECFRDL 53
DB 7 SAFSLGLLVMTAPPTPGPLAGDSDATNSLPLTSANKVEELIKYILGISALRREM 66
QY 54 CRTGICGILPEPAIFHLKLPAINDRHCGLIGFNESCLKADGFEFEVLFKFLTFTE 113
DB 67 CKFKKCEKSKALAEENLNLPKMAEKDCGSGFNQETCLMRITTGLEYQIYLDYQNE 126
QY 114 EFGKSVINVDVWELTKTGMDIOELNKLTKTHSPKPRDNGLGRLOGLK-YVVRHFA 173

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Db 127 N5CDKKNVSVHSTVILVOMLKSKVKNODEVTTPPTTDASIQAILQSDDEWLKHTTT 186
 Qy 174 FVYLAME---KFAGQAVRL 191
 Db 187 HLLRSLEDFLQPSLRVAVRM 207

RESULT 7
 Q9TH4 PRELIMINARY: PRT: 175 AA.

AC O9TH4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN-6 (FRAGMENT).
 GN IL-6.
 OS Actus nigriceps (black-headed night monkey).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Plimates; Platyrrhini; Cebidae; Aotinae; Aotus.
 OC NCBL_TaxID=57175;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Morillo L.A., Hernandez E., Echeverry S.J., Mendez J.A.,
 RA Patarroyo M.E.;
 RT "Actus nigriceps gene for IL-6";
 RL Submitted (Oct-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF097322; AAF21297.1; -
 DR HSSP: P05231; IALU.
 DR InterPro: IPR002069; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PRODOM: PD002435; -; 1.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 175 AA: 19205 MW: 28CCE57ACB99B189 CRC64;

Query Match 13.1%; Score 143; DB 6; Length 175;
 Best Local Similarity 28.7%; Pred. No. 2.4e-06;
 Matches 31; Conservative 25; Mismatches 52; Indels 0; Gaps 0;
 Qy 37 QRLNMLVNDCEFRDLCYRTGICGILEPAIFHLKLPAINDTDHGILGFNETSCLRK 96
 Db 55 KHLRYILEGISALRKELCDKSNMCESSQALAEKNINLIPMAEKDCFCGCFNEFCGLK 114
 Qy 97 LADGFEFEVLFKFLTTEFGKSVINVDVMEILLTKTGLGMDIOEELINKIT 144
 Db 115 ITTGLEFEVYLEYLNFRFESSKEQAGAVOMSTKGLIQSLQKAKNLS 162

RESULT 8
 Q9TH3 PRELIMINARY: PRT: 207 AA.
 AC Q9TH3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN-6.
 GN IL-6.
 OS Marmota monax (Woodchuck).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
 OC Marmota.
 OC NCBL_TaxID=9995;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PERIPHERAL BLOOD;
 RA Li D.H., Cullen J.M.;

RT "The Woodchuck Interleukin-6 Gene: Cloning and Structural Analysis."
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Li D.H., Cullen J.M.;

RT "Gene Structure of the Woodchuck Interleukin-6";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF012908; AAF34861.1; -
 DR EMBL: AF122896; AAF28873.1; -
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 SQ SEQUENCE 207 AA: 23645 MW: AD2F46E450E13470 CRC64;

Query Match 12.6%; Score 138; DB 11; Length 207;
 Best Local Similarity 21.0%; Pred. No. 9.2e-06;
 Matches 43; Conservative 45; Mismatches 97; Indels 20; Gaps 4;

Qy 5 KLSMLLVGSLVSGTGKLPDAPFEKDLILOR-----LMMMLVNDCE 50
 Db 2 KFSIASLGLLVAVAFPASELQREDEGNSVTRNKPTRASSCKTAGQISYILKEVEMR 61
 Qy 51 RDLCYRTGICGILEPAIF--HLKLPAINDTDHGILGFNETSCLKLAGFEFEVLF 108
 Db 62 KELCKNDENC--IKSHVAEENNNILPKMTBKDCGCPOTGYNRDNCLVRITSGLEPOVYL 119
 Qy 109 KFLTTF--GKSVINVDVMEILLTKTGLGMDIOEELINKITKTHVSPKFDNGLGRLOGLKY 166
 Db 120 RYINRKFQEGNNRDBRHHVQFSSKALIEIKQEVKDBNKIVFSPFANIMLAKLESND 179
 Qy 167 WVRHFAFYVLSAMEKFAQAVRL 191
 Db 180 WQVMTMQLILSNFEDFLQFTLRV 204

RESULT 9
 Q28403 PRELIMINARY: PRT: 207 AA.
 AC Q28403;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)
 DE INTERLEUKIN 6 (FRAGMENT).
 GN IL-6.
 OS Enhydra lutris (Sea otter).
 OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Mustellidae; Enhydra.
 OC NCBL_TaxID=34882;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96163018; PubMed=8575817;
 RA King D.P., Schrenzel M.D., McKnight M.L., Reidarson T.H., Hanni K.D.,
 RA Stolt J.L., Ferrick D.A.;
 RT "Molecular cloning and sequencing of Interleukin 6 cDNA fragments from
 the harbor seal (Phoca vitulina), killer whale (Orcinus orca), and
 Southern sea otter (Enhydra lutris nereis).";
 RL Immunogenetics 43:190-195(1996).
 DR EMBL: L46804; AAB01428.1; -
 DR HSSP: P05231; IL6.
 DR InterPro: IPR003573; -
 DR InterPro: IPR003574; -
 DR Pfam: PF00489; IL6; 1.
 DR PRINTS: PR00433; IL6GCSFMGF.
 DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN_6; 1.
 DR SMART: SM00126; IL6; 1.
 FT NON_TER 1
 SQ SEQUENCE 207 AA: 23527 MW: 729EE0CD91136D8B CRC64;

Query Match	12.5%	Score 136.5	DB 6	Length 207
Best Local Similarity	23.7%	Pred. No. 1.3e-05		
Matches	47	Conservative	41	Mismatches 89; Indels 21; Gaps
QY	12	VGSLVSGTRCKLP-----DA-----PEFEKDLIQRLNMLWVDECFRDLCTYRT	57	
DB	13	LGILLVMTAFPTPGPLGSDSKDQATSNRPPLTSADKMDKFEKILGKISALRNEMCDKX	72	
QY	58	GICKILPEPAIFHLKLAINDTDHCGILGFNETSCGCKKLADGFEFEVLEFPLTERCK	117	
DB	73	NKCGESKEVLENNINLPRLAKRDCFSRFQETCLRTITTGIOEQIHLVLESNNYG	132	
QY	118	SVINVDVVELLTKTLGMDIOEELNKLTKTHYSP-KPFDGCLGRLOGLKYVVRHFPASFV	176	
DB	133	NKDNASHVYISPKHLQLTLR-PMQIEVT--TPDPTDASLQALRKSDQKMLKHTTHILI	189	
QY	177	LSAME--KFGAGAVRL 191		
DB	190	LRRLEDLOFSLRATIRM 207		
RESULT	10			
ID	097535	PRELIMINARY;	PRT;	160 AA.
AC	097535			
DT	01-MAY-1999	(TREMBLrel. 10, Created)		
PR	01-MAY-1999	(TREMBLrel. 10, Last sequence update)		
DE	01-MAR-2001	(TREMBLrel. 16, Last annotation update)		
OS	INTERLEUKIN-6 (FRAGMENT).			
GN	IL-6.			
OC	Acute vociferans (noisy night monkey).			
CC	Eukaryota; Euteleostomi; Chordata; Vertebrata; Euteleostomi;			
NC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.			
LN	NCHL_TaxID=57176;			
RP	[1]			
RA	SEQUENCE FROM N.A.			
RT	Echeverry S.J., Hernandez E., Moreno A., Patarro M.E., Murtillo L.A.;			
FT	Identification, cloning and sequencing of different interleukin genes			
RL	in 4 Aotus species."			
DR	Submitted (JUL-1997) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF014505; AAD01531.1; -			
DR	HSSP; P05231; IL6.			
DR	InterPro; IPR003573; -			
DR	InterPro; IPR003574; -			
DR	Pfam; PF00489; IL6; 1.			
DR	PRINTS; PRO0433; IL6GSEPMGF.			
DR	PRINTS; PRO0434; INTERLEUKIN6.			
DR	PROSITE; PS00254; INTERLEUKIN_6; 1.			
DR	SMART; SM00126; IL6; 1.			
FT	NON_TER			
FT	1			
SO	SEQUENCE			
	160 AA; 17855 MW; 07A021338650A46D CRC64;			
Query Match	12.1%	Score 132;	DB 6;	Length 160;
Best Local Similarity	29.8%	Pred. No. 2.6e-05;		
Matches	28;	Conservative	21;	Mismatches 45; Indels 0; Gaps
QY	37	ORLNMWVDECFRDLCTYRTGICGILEPAAIFHLKLAINDTDHCGILGFNETSCLK	96	
DB	55	KHIRILGIALRLKREICDKSNMSSSKALANNINLPKMAKDGCGSGNETETCLK	114	
QY	97	LADGFEFEVLEFPLTERGKSVINVDVVELTK 130		
DB	115	ITTGLEFEVLEYLQNRFESSKEGAGAVOMTK 148		
RESULT	11			
ID	09WV08	PRELIMINARY;	PRT;	210 AA.
AC	09WV08			
DT	01-NOV-1999	(TREMBLrel. 12, Created)		

DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)
DT	01-MAR-2001	(TREMBLrel. 16, Last annotation update)
DE	IL-6 (FRAGMENT)	
OS	Mesocricetus auratus (Golden hamster).	
OC	Euxaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;	
OC	Mesocricetus.	
OX	NCBI_TaxID=10036;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN-APA; TISSUE=KIDNEY;	
RA	Nishida E.;	
RT	*Apa hamsters IL-6 partial cDNA.*;	
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.	
DR	HSSP: AB028635; BAA78766.1; -	
DR	HSSP: P05231; IALU	
DR	InterPro: IPR003573; -	
DR	InterPro: IPR003574; -	
DR	Pfam: PF00489; IL6; 1.	
DR	PRINTS: PRO0433; IL6GCSFMGF.	
DR	PRINTS: PRO0434; INTERLEUKIN6.	
DR	PROSITE: PS00254; INTERLEUKIN_6; 1.	
DR	SMART: SM00126; IL6; 1.	
FT	NON_TER	1
SO	SEQUENCE	210 AA; 24060 MW; BD9319AFEB913AB3 CRC64;
Query Match	11.88; Score 129.5; DB 11; Length 210;	
Best Local Similarity	24.98; Pred. No.6.4e-05;	
Matches	52; Conservative 33; Mismatches 83; Indels 41; Gaps	
QY	9 LLVGLSLVSGTRGKRLDPAP-----EPEKDLLIQ-----INMMLMVIDECFRD 52	
Db	10 LVFGLILLVMAT--ALPTQVRGDEFTETPNRPVYTTSQVGLVTVYLRREYLRKE 67	
QY	53 LCYRTGCGCKG----ILEPAALFHLKILPAINDTDHCGILGFNETSCGLKADGFEFEVLF 108	
Db	68 LCNNPNCGMNDVYALEN---NLPLPVIOINDGLODTGYMWEICLLKRTISGLDYOYL 133	
QY	109 KELTTEFGKSYINVD-----VMELETKITLGDIOELNKLKTKTHYSPKFDRCGLGR 160	
Db	124 EGVTV-----NVQDNKKDKARVIGSPITKLSIFRQVWVGPKKIYTPSPTSKAILMEK 176	
QY	161 LQGLKYNVRRHFASTFYVLSAMKEFAGQAVR 189	
Db	177 LESQKEMPRRTKIRLIKALKEEFLEVTVMR 205	
RESULT	12	
Q9MZRL	PRELIMINARY:	PRT: 241 AA.
ID	Q9MZRL	AC
DT	01-OCT-2000 (TREMBLrel. 15, Created)	
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DE	01-MAR-2001 (TREMBLrel. 16, Last annotation update)	
DE	INTERLEUKIN 6.	
OS	Oryctolagus cuniculus (Rabbit).	
OC	Euxaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	
OX	NCBI_TaxID=9986;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=SPLEEN, LYMPH NODE;	
RA	MEDLINE=20304414; PubMed=10843729;	
RT	Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;	
RT	*The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the	
RT	European rabbit (Oryctolagus cuniculus).*	
RL	Cytokine 12:555-565(2000)	
DR	EMBL: AF1691176; AAR66660.1; -	
DR	InterPro: IPR003573; -	
DR	InterPro: IPR003574; -	
DR	Pfam: PF00489; IL6; 1.	
DR	PRINTS: PRO0433; IL6GCSFMGF.	

DR PRINTS: PR00434; INTERLEUKIN6.
 DR PROSITE: PS00254; INTERLEUKIN6; UNKNOWN.1.
 DR SMART: SM00126; IL6; 1.
 DR SEQUENCE 241 AA; 27021 MW; 781D323692C3EE97 CRC64;

Query Match 10.6%; Score 116.5; DB 6; Length 241;
 Best Local Similarity 22.7%; Pred. No. 0.0014;
 Matches 41; Conservative 30; Mismatches 99; Indels 11; Gaps 3;

OY 18 SCFRGKLPDAPEFEKDLQILMMMLVDECFRDLGICFRGICGLLEPAIFHLKPAI 77
 DB 37 SNTKAS-PKRTLPRTPTIESISLETIKELAKEMCDIDVNCMKREKALAEVNLHLPRL 95
 OY 78 NDTDHGCLIGFNETSCLIKLADGFEFEVLKFLTTEFGKSVINVDV-----MELLTKT 131
 DB 96 IEDGCFPAVNNETCLRTITSGLMERBYLHLQAKFRDEDENTFVSNVLYKNIQHLIKT 155
 OY 132 LGHDIOBELNKLTKTHYSPKFRGLGLRGLGKIYVRIEASTYVLSAMEKFGQAVRVL 191
 DB 156 L---SPKYNMLNEATLKPAAVAVSLMENLQKNMKITTTIIFILRGILNPLEFTLRAY 211
 OY 192 D 192
 DB 212 D 212

RESULT 13
 OY0UKF6 PRELIMINARY: PRT: 684 AA.

AC 09UKF6: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73 KDA SUBUNIT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEPATOCELLULAR CARCINOMA;
 RA Yu S., Chen W., Pang X., Dong X., Wang H.;
 RT "Homo sapiens mRNA for CPSP (cleavage and polyadenylation specificity factor) 73 kDa subunit."
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF171877; AAF00224.1; -
 DR InterPro: IPR001279; -
 DR Pfam: PF00753; lactamase_B.1.
 DR SEQUENCE 684 AA; 77485 MW; F8AA24EAFB78377 CRC64;

Query Match 8.7%; Score 95; DB 4; Length 684;
 Best Local Similarity 25.3%; Pred. No. 0.68;

Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILPPAI-----PHUKLPAINDTDHCG-LIGFNETSCLIKLADGFEFEVLKFLTTE 114
 DB 58 LIDPAEIDLILSHFHL-----DHGCLPWFLOKTSKGRFTPMTHAKAIYRWLSD 109
 OY 115 FGR-SVINVDVMEELTKTLGMDIOBELNKLTKTHYSPKFRDRLGLRGLGKIYVRIEASTYVLSAMEKFGQAVRVL 173
 DB 110 YKAVSNISADDM-LYETET---DLESMDKIETINFHEVK-----EVAGIKFMCYH--A 156
 OY 174 FYVLSA---MEKFAQAVRVL-----DSIPDVPDV 201
 DB 157 GHVLGAMFMIEIAG--VKLLYTGDFSROEDRHLMAAETIPNIPDI 200

RESULT 14
 ID P79101 PRELIMINARY: PRT: 684 AA.
 AC P79101;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR PROTEIN.
 GN CPSP.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=97078135; PubMed=8929409;
 RA Jenny A., Manville-Sebastia L., Preker P.J., Keller W.;
 RT "Sequence similarity between the 73-kilodalton protein of mammalian CPSP and a subunit of yeast polyadenylation factor I."
 RL Science 274:1514-1517(1996).
 DR EMBL: X85906; CAA55151.1; -
 DR InterPro: IPR001279; -
 DR Pfam: PF00753; lactamase_B.1.
 DR SEQUENCE 684 AA; 77487 MW; 17A0CAFED2B8172E CRC64;

Query Match 8.7%; Score 95; DB 6; Length 684;
 Best Local Similarity 25.3%; Pred. No. 0.68;
 Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILPPAI-----PHUKLPAINDTDHCG-LIGFNETSCLIKLADGFEFEVLKFLTTE 114
 DB 58 LIDPAEIDLILSHFHL-----DHGCLPWFLOKTSKGRFTPMTHAKAIYRWLSD 109
 OY 115 FGR-SVINVDVMEELTKTLGMDIOBELNKLTKTHYSPKFRDRLGLRGLGKIYVRIEASTYVLSAMEKFGQAVRVL 173
 DB 110 YKAVSNISADDM-LYETET---DLESMDKIETINFHEVK-----EVAGIKFMCYH--A 156
 OY 174 FYVLSA---MEKFAQAVRVL-----DSIPDVPDV 201
 DB 157 GHVLGAMFMIEIAG--VKLLYTGDFSROEDRHLMAAETIPNIPDI 200

RESULT 15

ID O90XK7 PRELIMINARY: PRT: 684 AA.

AC 090XK7: 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
 DE CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR 73 KDA SUBUNIT.
 GN CPSP3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/C;
 RA Wang H., Chen W., Yu S., Xie L.;
 RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF203969; AAF19420.1; -
 DR MGI: 1859328; Cpaf3.
 DR InterPro: IPR001279; -
 DR Pfam: PF00753; lactamase_B.1.
 DR SEQUENCE 684 AA; 77528 MW; 00302767EDF076F CRC64;

Query Match 8.7%; Score 95; DB 11; Length 684;
 Best Local Similarity 25.3%; Pred. No. 0.68;

Matches 42; Conservative 33; Mismatches 41; Indels 50; Gaps 11;

OY 63 ILPPAI-----PHUKLPAINDTDHCG-LIGFNETSCLIKLADGFEFEVLKFLTTE 114
 DB 58 LIDPAEIDLILSHFHL-----DHGCLPWFLOKTSKGRFTPMTHAKAIYRWLSD 109

Qy 115 FCK-SVINVDVMEIITKTIGMDIOELNKLTKTHYSPKFDRLGLGRLQGLKTYWRHPAS 173
Db 110 YVKVSNISADDM-LYTEP---DLESMDKIEFINPHEVK-----EVAGIKFWCYH--A 156
Qy 174 FYVLSA---MEKFAQAVRVL-----DSIPDTPDV 201
Db 157 GHVLGAAMFMEIING--VKLLYTGDESRQEDRHLMAEIPNKPDI 200

Search completed: October 4, 2001, 19:11:56
Job time: 1182 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 17:19:19 ; Search time 76.54 Seconds
(Without alignments)
5020.588 Million cell updates/sec

Title: US-09-230-048-1

Perfect score: 612
Sequence: 1 ATGCTGCTGTCAGTGTG.....CTCCTGACGTCACGATAG 612

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: /SIDSI/gcgdata/geneseq/NA1980.DAT:*
2: /SIDSI/gcgdata/geneseq/NA1981.DAT:*
3: /SIDSI/gcgdata/geneseq/NA1982.DAT:*
4: /SIDSI/gcgdata/geneseq/NA1983.DAT:*
5: /SIDSI/gcgdata/geneseq/NA1984.DAT:*
6: /SIDSI/gcgdata/geneseq/NA1985.DAT:*
7: /SIDSI/gcgdata/geneseq/NA1986.DAT:*
8: /SIDSI/gcgdata/geneseq/NA1987.DAT:*
9: /SIDSI/gcgdata/geneseq/NA1988.DAT:*
10: /SIDSI/gcgdata/geneseq/NA1989.DAT:*
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21: /SIDSI/gcgdata/geneseq/NA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/NA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	612	AAV04630	Human herpesvirus
2	612	100.0	615	AAV54070	Kaposi sarcoma her
3	612	100.0	615	AAV10243	Human herpesvirus
4	612	100.0	35100	AAV73802	KSHV LTR DNA (nucl
5	612	100.0	137507	AAV19941	KSHV long unique c
6	61	10.0	555	AAV4359	CDNA encoding huma
7	54.6	8.9	555	AAV32818	Interleukin-6 codi
8	54.6	8.9	593	AAV63359	Human interleukin
9	54	8.8	1260	AAZ09202	Human IL-6 recepto
10	53.6	8.8	564	AAO55689	Full length interl
11	53.6	8.8	564	AAO55691	Full length interl

12	53	8.7	486	AA257444	Human interleukin
13	53	8.7	525	AAO70446	Human interleukin
14	53	8.7	555	AAO00977	Segment of human B
15	53	8.7	555	AAV44357	CDNA encoding huma
16	53	8.7	555	AAV44356	Human interleukin
17	53	8.7	555	AAV44360	Human interleukin
18	53	8.7	555	AAV44358	CDNA encoding huma
19	53	8.7	560	AAO03365	Segment of human B
20	53	8.7	561	AAO27479	Encodes human IL-6
21	53	8.7	561	AAO56903	Human interleukin
22	53	8.7	561	AAO90773	Human interleukin
23	53	8.7	566	AAO80300	Interleukin 6. A
24	53	8.7	639	AAV91706	Human interleukin
25	53	8.7	663	AAV64947	Human interleukin
26	53	8.7	1099	AAO25831	Mutant human BCDP
27	53	8.7	1101	AAO80965	Plasmid pBSF2-18.
28	53	8.7	1101	AAO81517	Sequence encoding
29	53	8.7	1101	AAO90131	DNA sequence of PB
30	53	8.7	1101	AAO90135	DNA sequence of PB
31	53	8.7	1101	AAO90345	Plasmid pBSF2-18,
32	53	8.7	1102	AAO21360	Human low adenosin
33	53	8.7	1102	AAO35238	Human adenosine re
34	53	8.7	1113	AAV21361	Human low adenosin
35	53	8.7	1113	AAO35239	Human adenosine re
36	53	8.7	1139	AAO80299	Interleukin 6. A
37	53	8.7	1139	AAO90255	Interleukin-6. Ho
38	53	8.7	1161	AAO81460	Sequence encoding
39	53	8.7	1162	AAO01763	BSF-2 gene for hum
40	53	8.7	1162	AAO11824	B cell differentia
41	53	8.7	1165	AAO56265	Sequence of human
42	53	8.7	1545	AAV07073	IL-6R/IL-6 fusion
43	53	8.7	1552	AAV97849	Human fusion poly
44	53	8.7	1627	AAV97848	Human fusion poly
45	53	8.7	2759	AAV21362	Human low adenosin

ALIGNMENTS

RESULT 1	AAV04630 standard; DNA: 612 BP.
ID	AAV04630
XX	AAV04630:
AC	01-JUL-1998 (first entry)
XX	
DE	Human herpesvirus 8 Interleukin-6 gene.
XX	
KW	ds; Interleukin-6; IL-6; human herpesvirus 8; HHV8;
RW	shotgun-cloning; Antibody; diagnosis; treatment.
XX	
OS	Human herpesvirus 8.
XX	
FT	Key
FT	Location/Qualifiers
FT	1..612
FT	/*tag= a
FT	/product= Interleukin-6
FT	/note= "no stop codon given at 3'end"
XX	
XX	WO9803657-A1.
XX	
XX	29-JAN-1998.
XX	
XX	19-JUL-1996; 96WO-EP03199.
XX	
XX	19-JUL-1996; 96WO-EP03199.
XX	
XX	(BEHW) BEHRING DIAGNOSTICS GMBH.
XX	(UBNY) UNIV NEW YORK STATE.
XX	
XX	Albrecht J, Fleckenstein B, Friedman-Klen A, Huang Y;
PI	Neipel F;


```
|||||
Db 181 aaggatcttcagagcccgctgctatttctcatctgaactacagcacaagatact 240
OY 241 GATCAGCGGCTTAATAGATTAAAGACTAGTGCCTTAATAAGCTGCGGATGGC 300
Db 241 gatacgcggygttaataagatttaagactagctgcttaaaagctgcgcaagc 300
OY 301 TTTTGTGAATTCGAGGTGTTGTTAACTTTTAAACGACGAGTTTGAATAATCAGTATA 360
Db 301 ttlttgatctcgagtgctgtttaaagttttaaagcagcggtttgaaatacgtgata 360
OY 361 AACGTGACGTCATGAGAGCTTTCACGACGACTTACGATGGACATACAGAGAGCTC 420
Db 361 aacgtgacgctcatgagactctcagcaagacctagatgagacatacagaagagctc 420
OY 421 AATTAAGTGACTAAGACGACATACAGTCACCAATTTGACGCGGCTTTTGGGAGG 480
Db 421 aataagctgactaagaagcactacacacacccaatttgccgcygctactatggagag 480
OY 481 CTTCAGGAGCTTAAATGATTTGGGTGACACACTTTCCTTCTGTTTATGTTGAGTCAATG 540
Db 481 cttaagcgactaagatattgggtgagacacttgcttcgtttaaagtctgagtgcaatg 540
OY 541 GAAAGCTTTGACAGTCACAGCGGCTGCTTTTGGACTCTATCCACAGCTGACCTGAC 600
Db 541 gaaagctttgacagtcacagcggtgctgttctgactctacccagacgctgacctgac 600
OY 601 GTCCACGATAG 612
Db 601 gtccacgataag 612
```

RESULT 3

AAV10243 standard; DNA: 615 BP.

AAV10243:

15-JUL-1998 (first entry)

Human herpesvirus 8 (HHV-8) divergent locus DL-B probe 4.

DL-B; thymidylate synthase; dihydrofolate reductase; probe: HHV-8;
Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
Kaposi's sarcoma; beta-chemokine-like; hybridisation; VII-6; ss.

Synthetic.

Kaposi's sarcoma associated herpesvirus.

WO9804284-A1.

05-FEB-1998.

24-JUL-1997; 97WO-US12931.

25-JUL-1996; 96US-0022591.

(UJJO) UNIV JOHNS HOPKINS.

Hardwick JM, Hayward GS, Nicholas J, Reitz MR;

WPI; 1998-130422/12.

New human herpes virus gene region containing 8 open reading frames
PT - useful for, e.g. diagnosing Kaposi's sarcoma or body cavity based
PT large cell lymphoma

Claim 4; Page 53; 84pp; English.

The present probe was synthesised for detecting human herpesvirus-8
CC (HHV-8) divergent locus DL-B which lies between open reading frames
CC 11 and 17. Sequencing of the HHV-8 divergent locus DL-B revealed
CC the presence of nine viral ORFs with gene products related to cellular

CC proteins. These proteins include the thymidylate synthase (TS),
CC dihydrofolate reductase (DHFR), Bcl-2 homologue, IE-1A, IE-1B and,
CC four cytokines which include viral interleukin-6 (vIL-6), viral
CC macrophage inhibitory protein (vMIP)-1A and -1B and beta-chemokine-like
CC (BCK) protein. The sequences of these proteins are given in
CC AAW40100-W40108. The invention claims the mentioned proteins and a
CC polynucleotide containing HHV-8 genes encoding one or more of these
CC proteins. The invention also claims that the polynucleotide and the
CC proteins may be used directly or indirectly, e.g. using antibodies to
CC the proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's
CC sarcoma, Castleman's disease, multiple myeloma and body cavity based
CC large cell lymphoma (BCL). The proteins have also been claimed to be
CC useful in screening compounds for drugs to treat HHV-8 diseases.

SO Sequence 615 BP; 150 A; 129 C; 162 G; 174 T; 0 other;

Query Match 100.0%; Score 612; DB 19; Length 615;
Best Local Similarly 100.0%; Pred. No. 6, 2e-201;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 ATGTCGTGTCAGATGTTGCTCTCTGCTGCTGCTTACATGCTGCTATCTGAAAG 60
Db 1 atgtcgtgtcaagatgtgtgtctctctctgtgtgtgttcaatcgtgtatctgaaag 60
OY 61 CGGGGCAAGTTGCCGAGACGCCCGAGTTTGAAAAGATCTTTCATTCAGAGACTCAAT 120
Db 61 cggggcaagttgccgagacgcccgagtttgaaaagatcttccatcagagactcaat 120
OY 121 TGAATCTGATGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 tgaatctgatgagatgagatgagatgagatgagatgagatgagatgagatgagatgag 180
OY 181 AAGGATATCTAGAGCCCGCTGATTTTATGTCGAACATACAGCATCAAGATGACT 240
Db 181 aaggatattctagagcccgctgattttatgtcgaacatcacagcatcaagatgact 240
OY 241 GATCAGCGGCTTAATAGATTAAAGACTAGTGCCTTAATAAGCTGCGGATGGC 300
Db 241 gatacgcggygttaataagatttaagactagctgctttaaagctgcgcaagc 300
OY 301 TTTTGTGAATTCGAGGTGTTTAACTTTTAAACGACGAGTTTGAATAATCAGTATA 360
Db 301 ttlttgatctcgagtgctgtttaaagttttaaagcagcggtttgaaatacgtgata 360
OY 361 AACGTGACGTCATGAGAGCTTTCACGACGACTTACGATGGACATACAGAGAGCTC 420
Db 361 aacgtgacgctcatgagactctcagcaagacctagatgagacatacagaagagctc 420
OY 421 AATTAAGTGACTAAGACGACATACAGTCACCAATTTGACGCGGCTTTTGGGAGG 480
Db 421 aataagctgactaagaagcactacacacccaatttgccgcygctactatggagag 480
OY 481 CTTCAGGAGCTTAAATGATTTGGGTGACACACTTTCCTTCTGTTTATGTTGAGTCAATG 540
Db 481 cttaagcgactaagatattgggtgagacacttgcttcgtttaaagtctgagtgcaatg 540
OY 541 GAAAGCTTTGACAGTCACAGCGGCTGCTTTTGGACTCTATCCACAGCTGACCTGAC 600
Db 541 gaaagctttgacagtcacagcggtgctgttctgactctacccagacgctgacctgac 600
OY 601 GTCCACGATAG 612
Db 601 gtccacgataag 612
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RESULT 4

AAV73802/C standard; DNA: 35100 BP.

AAV73802:

25-FEB-1999 (first entry)


```

PN MO9634104-A1.
XX
XX 31-OCT-1996.
XX
XX 26-APR-1996: 96MO-IT00084.
XX
XX 28-APR-1995: 95IT-0RM0273.
XX
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX
XX Ciliberto G, Paonessa G, Savino R;
XX
XX WPI: 1996-497635/49.
XX
XX P-PSDB; AAM07200.
XX
XX New human interleukin-6 antagonists - incapable of binding gp 130,
XX
XX used for treating e.g. multiple myeloma, arthritis or osteoporosis
XX
XX
XX Claim 1: Page 21-22; 30pp; English.
XX
XX ANT44359 encodes Sant7, a human interleukin-6 (IL-6) antagonist. Sant7
XX
XX and other IL-6 antagonists (AAM07197-199) are characterised in that they
XX
XX are totally incapable of binding gp130. Mutations were introduced into
XX
XX four codons in the region coding for IL-6 cloned into
XX
XX pT7.7/IL-6/DFRD/Hind, creating the following amino acid substitutions:
XX
XX Y31D, G35F, S118R and V121D. These mutations drastically reduced the
XX
XX biological activity of the cytokine, without altering its ability to bind
XX
XX to the IL-6 receptor, thus generating IL-6 DFRD (see AAM07201). Sant7
XX
XX was generated from Sant5 (contg. 5 extra mutations: Q75Y, S76K, Q175I,
XX
XX S176R and Q183A) by inserting 3 more amino acid substitutions: L57D, E59F
XX
XX and N60W. The IL-6 antagonists can be used for the prepn. of
XX
XX pharmaceutical cpds. for the treatment of multiple myeloma, rheumatoid
XX
XX arthritis, lupus erythematosus and osteoporosis.
XX
XX
XX Sequence 555 BP; 178 A; 140 C; 130 G; 106 T; 1 U; 0 other:
SQ
Query Match 10.0%; Score 61; DB 17; Length 555;
Best Local Similarity 47.3%; Pred. No. 7, 6e-11;
Matches 184; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
OY 160 TGTACCGTACCCGATCCTGCAAGGCTATTCTAGACCCCGCTGTTATTTTCATCTGAAA 219
DB 130 tgtacccgagagtaacatgtgtgaaagcagaagaagccgacgcatctcggaaaccggaac 189
OY 220 CTACACGACCATCAAGACTGATCTACTCGGGGTTAATAGATTATAGACTAGCTGC 279
DB 190 ctccaaagaagtcgtgaaagaagcagtcctctcaaaagattcaatgaggaacttcg 249
OY 280 CTTAAAAACCTCCCGCATGGCTTTTTCGAAATTCGAGCTGTGTTTAAGTTTAAAGCAGC 339
DB 250 ctggagaaatcatcactcgtgctcttcgagtttgaagttacctaagaatcctccagaac 309
OY 340 GAGTTTGCATAATCATCTGATTAACGTCGACGTCATGACCTTCTGAGGAAGACTTAGCA 399
DB 310 agatttggagagtgatgagaaacagcagagcgtctccaaatgagcgaagcccgatc 369
OY 400 TGGGACATACAGAGAGAGTCAATTAAGCTGACTAAGACGCACTACAGTCCACCAAAATT 459
DB 370 cagttctcctgcaaaaaagaaagaaatctagatgcaataacccccctgaccaaacaca 429
OY 460 GACCCGGCTCTATTAGGAGAGCTTTCAGGACCTTAATTTGGTGGACACTTTGCTTCG 519
DB 430 gatgcagagctcgtcagagagctcagagcagaaacagtgagtcgaggaacatgacaact 489
OY 520 TTTTATGTTCTGAGTCCAAATGGAAGTT 548
DB 490 catctcatctcgtcagagccttaagaagtc 518
RESULT 7
AAT32818
ID AAT32818 standard; cDNA; 555 BP.

```

```

XX
XX AAT32818;
XX
XX 24-FEB-1997 (first entry)
XX
XX Interleukin-6 coding sequence.
XX
XX Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
XX
XX bovine; granulocyte colony stimulating factor; bG-CSF; receptor; gp130;
XX
XX thrombocytopoiesis; haematopoietic progenitor cell; rheumatoid arthritis;
XX
XX bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
XX
XX breast cancer; infectious disease; bone marrow progenitor cell; therapy;
XX
XX postmenopausal osteoporosis; systemic lupus erythematosus; hormone; ss.
XX
XX Homo sapiens.
XX
XX MO9618648-A1.
XX
XX 20-JUN-1996.
XX
XX 13-DEC-1995: 95MO-IT00216.
XX
XX 14-DEC-1994: 94IT-0RM0805.
XX
XX (RICE-) IST RICERCHIE BIOL MOLECOLARE ANGELETTI.
XX
XX Ciliberto G, Lahm A, Savino R, Toniattti G;
XX
XX WPI: 1996-300575/30.
XX
XX P-PSDB; AAM02609.
XX
XX Identifying interleukin-6 super-agonists and (super)antagonists -
XX
XX using a 3-dimensional model of bovine granulocyte colony stimulating
XX
XX factor to identify binding sites
XX
XX
XX Example 1: Page 13-14; 26pp; English.
XX
XX
XX This sequence represents the cDNA encoding human interleukin-6 (IL-6).
XX
XX Superagonists, antagonists, and superantagonists of the encoded IL-6
XX
XX protein can be identified using the method of the invention. The method
XX
XX comprises comparing the encoded protein with the sequence of the bovine
XX
XX granulocyte colony stimulating factor (bG-CSF). On the basis of this
XX
XX comparison a 3-dimensional model of the IL-6 is formulated, which allows
XX
XX the identification of residues that form the site of interaction with the
XX
XX specific receptor, and those that constitute the site of interaction with
XX
XX gp130. The IL-6 superagonists identified by this method can be used for
XX
XX the treatment of thrombocytopoiesis, and for the ex vivo expansion of
XX
XX human haematopoietic progenitor cells for bone marrow transplantation and
XX
XX gene therapy. They can also be used for the treatment of breast cancer,
XX
XX leukaemia, and infectious diseases or diseases connected with disorders
XX
XX of bone marrow progenitor cells. The antagonists and superantagonists
XX
XX characterised by the method can be used for the treatment of diseases
XX
XX characterised by the overproduction of IL-6, particularly multiple
XX
XX myeloma, rheumatoid arthritis, postmenopausal osteoporosis, and systemic
XX
XX lupus erythematosus. The method can also be used to identify IL-6
XX
XX variants with a greater affinity for the specific receptor, or variants
XX
XX with a reduced or abolished affinity for gp130.
XX
XX
XX Sequence 555 BP; 182 A; 136 C; 129 G; 107 T; 1 other:
SQ
Query Match 8.9%; Score 54.6; DB 17; Length 555;
Best Local Similarity 46.3%; Pred. No. 1, 2e-08;
Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;
OY 160 TGTACCGTACCCGATCCTGCAAGGCTATTCTAGACCCCGCTGTTATTTTCATCTGAAA 219
DB 130 tgtacaaagagtaacatgtgtgaaagcagaagaagcctcggaaacaaaccggaac 189
OY 220 CTACACGACCATCAAGACTGATCTACTCGGGGTTAATAGATTATAGACTAGCTGC 279
DB 190 ctccaaagaagtcgtgaaagaagtcgtctccaaatcgtgattcgaatgaggaacttcg 249

```


DE	Full length interleukin-6 gene encoding FI71L L175M mutation.
XX	IL-6; carboxy terminal mutants; mutants; proliferation;
KW	differentiation; immunotherapeutic; antiinflammatory;
KW	thrombocytopenia; chemotherapy; bone marrow transplant; ss.
XX	
OS	Homo sapiens.
XX	
XX	Key
XX	Location/Qualifiers
XX	523..525
XX	mutation
XX	/*tag= a
XX	/note= "codon for Leu 175 mutated to encode Met"
FT	511..513
FT	mutation
FT	/*tag= b
FT	/note= "codon for Phe 171 mutated to encode Ieu"
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XX	W09402512-A.
XX	
XX	03-FEB-1994.
XX	
XX	23-JUL-1993; 93WO-US06928.
XX	
XX	23-JUL-1992; 92US-0918181.
XX	
XX	(UNCL-) UNIV NORTH CAROLINA.
XX	
XX	FOIWKES D:
XX	
XX	WPI: 1994-048796/06.
XX	P-PSDB: AAR45720.
XX	
XX	New carboxy terminal interleukin-6 mutants - having amino acid
XX	substituents at position 171 or 175, for use in immunotherapeutic or
XX	anti-inflammation comps.
XX	
XX	Claim 1; Fig 4; 79pp; English.
XX	
XX	The sequence shows the gene encoding full length L175M FI71L mutant
XX	interleukin 6. It has been found that mutants of IL-6 having amino
XX	acid substituents at amino acid 171 or 175 have increased activity over
XX	the wild type sequence. The IL-6 mutants are useful in
XX	proliferation of B cells, T cells, megakaryocytes and multi-
XX	potential haematopoietic progenitor cells and they also induce
XX	various acute phase proteins in liver cells. They are useful in
XX	immunotherapeutic and antiinflammation comps. They can also be
XX	used for the treatment of patients suffering from thrombocytopenia
XX	or undergoing chemotherapy or bone marrow transplant.
XX	See also A055688-92.
XX	
XX	Sequence 564 BP; 184 A; 132 C; 132 G; 116 T; 0 other;
XX	
XX	Query Match 8.8%; Score 53.6; DB 15; Length 564;
XX	Best Local Similarity 45.5%; Pred. No. 2.7e-08;
XX	Matches 191; Conservative 0; Mismatches 229; Indels 0; Gaps 0;
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XX	154 GACCTCTGTTACCCGACCGCATCTGCAAGGCTATTCTAGACCCGCGCTATTATTTTCAT 213
XX	DB 127 gagaccttaacaagaagtaacatcgtgtgaagaagcaataaagaagcctgcagaaaaaac 186
XX	214 CTGAACACTACGACGCATCAACGATCTACTGATCGGGTTAATAGATTATAGACT 273
XX	DB 187 ctgaaccttcagaagaatcgtcgtgaagaatgtgtttcctaactcgtatcctaagtga 246
XX	274 AGCTCCCTTTAAAAAGCTCGCCGATGGCTTTTGTGAATTGAGAGTGTTGTTTAAGTTT 333
XX	DB 247 actgtctcgtgtgaagaatcacaagccttcttggaatttgaggtacactagatcacc 306
XX	334 ACGAGCGAGTTTGGAAAAATCACTGATTAACGTCGACGTCATGACGCTTGTGACGAAGAC 393
XX	DB 307 cagaacagatttgagagtagtgaggaagacagagagctgtctcagaatgtgcaccaaagtc 366
XX	394 TTAGATGGGACATCAAGAGAGGCTCAATAAGCTGACTAAGACGACATACAGTCCACCC 453

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Db      357  cTgATccagcttcttctcagaanaaaagcacaataatcagatgcaataaccacccgagatcca 426
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Db      427  accacaatatcgagcctctctgacgaagctgcagcagcaagaaccagtgctcgaagacatg 486
Oy      514  GCTTGCTTTTATGTTCTGAGTCGAATGGAAMAGTTTTCGACGTCAAGCGGTGCGTGTTCG 573
Db      487  acaactcatctatctctgagatcttctgaaagaattcatgcagctccctccgtgctctgc 546

RESULT 12
ID      AA557444
AC      AA557444 standard; DNA; 486 BP.
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XX      AA557444;
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XX      10-APR-2000 (first entry)
XX
XX      Human interleukin 6 DNA sequence.
XX
XX      Homo sapiens.
XX
XX      CN1203920-A.
XX
XX      06-JAN-1999.
XX
XX      12-MAY-1998; 98CN-0101871.
XX
XX      12-MAY-1998; 98CN-0101871.
XX
XX      (Still/) SI L.
XX
XX      SI L;
XX
XX      WPI; 2000-106829/10.
XX
XX      Producing recombinant human interleukin-6 - comprises e.g. artificial
XX      synthesis of up-stream and downstream oligonucleotide primers
XX
XX      Example 1; Page 3; 13pp; Chinese.
XX
XX      The present invention describes a method used for the production of
XX      recombinant human interleukin-6 (rhIL-6). The method comprises:
XX      artificial synthesis of up-stream and downstream oligonucleotide
XX      primers; using human IL-6 DNA gene as template and using the described
XX      primers to make PCR amplification; using EcoRI and BamHI to respectively
XX      enzyme-cut pBV220 plasmid and PCR amplified rhIL-6 gene fragment, then
XX      using T4DNA ligase to make connection; using the formed expression
XX      plasmid to convert colibacillus, inducing and culturing the formed
XX      transformant and recovering rhIL-6 from the culture and purifying it.
XX      The protein expressed by transformant in this method can be 45% of
XX      total protein of thallus, and the purity of rhIL-6 can be above 95%.
XX      The present sequence represents rhIL-6, as given in the present invention.
XX
XX      Sequence 486 BP; 158 A; 113 C; 117 G; 98 T; 0 other;

Query Match      8.7%; Score 53; DB 21; Length 486;
Best Local Similarity 46.0%; Pred. No. 4; le-08;
Matches 179; Conservative 0; Mismatches 210; Indels 0; Gaps 0

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Oy      220  CTACCGGACCATCAACATCTGATCTGCTCGGGTTTATATGATTTTATGAGACTAAGTCG 279
Db      121  ctTccaaagaatgctgtaaaaagaatgagatcttcccaatctgagatccaatgagagacttgc 180

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: October 4, 2001, 16:49:19 ; Search time 1228.55 seconds
(without alignments)
7705.232 Million cell updates/sec

Title: US-09-230-048-1

Perfect score: 612
Sequence: 1 ATGCGCTGCTTCACGTTGTG.....CTCCAGACGTCACGATAG 612

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 773874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_ba3:*
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8: gb_ov:*
9: gb_pat1:*
10: gb_pat2:*
11: gb_ph:*
12: gb_pl1:*
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96: gb_v49:*
97: gb_v50:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	100.0	612	9 A68629	A68629 Sequence 1
2	612	100.0	612	59 KSU73655	U73655 Kaposi's sa
3	612	100.0	615	9 AR030968	AR030968 Sequence
4	612	100.0	615	9 AR069034	AR069034 Sequence
5	612	100.0	615	59 KSU67774	U67774 Kaposi's sa
6	612	100.0	6600	59 KSU71365	U71365 Kaposi's sa
7	612	100.0	35100	9 AR065849	AR065849 Sequence
8	612	100.0	137508	59 KSU75698	U75698 Kaposi's sa

9	607.2	99.2	133661	59	U93872
10	61	10.0	555	9	A57729
11	61	10.0	555	9	AR082470
12	56.2	9.2	639	91	CEYIN6A
13	54.6	8.9	555	9	AA2034
14	54.6	8.9	555	9	A11824
15	54.6	8.9	555	9	AR021247
16	54.6	8.9	555	9	AR064654
17	54.6	8.9	555	9	AR070274
18	54.6	8.9	593	10	AX084328
19	54.6	8.9	639	97	MACIN6A
20	54.6	8.9	683	85	AB000554
21	54	8.8	1260	10	E28089
22	53.6	8.8	564	10	E28089
23	53.6	8.8	564	10	127637
24	53.4	8.7	628	88	AF097323
25	53	8.7	555	9	A57723
26	53	8.7	555	9	A57726
27	53	8.7	555	9	A57727
28	53	8.7	555	9	A57728
29	53	8.7	555	9	AR082464
30	53	8.7	555	9	AR082467
31	53	8.7	555	9	AR082468
32	53	8.7	555	9	AR082469
33	53	8.7	555	10	E02172
34	53	8.7	560	10	E02170
35	53	8.7	561	10	E52043
36	53	8.7	566	10	I08634
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42	53	8.7	1098	93	HSILB2R
43	53	8.7	1101	9	A10873
44	53	8.7	1101	9	A11845
45	53	8.7	1101	9	A13367

ALIGNMENTS

U93872 Kaposis's sarcoma
AR082470 Sequence 7
L26032 Cercaricobus
A42034 Sequence 1
A51824 Sequence 1
AR012247 Sequence
AR064654 Sequence
AR070274 Sequence
AR084338 Sequence
L26028 Macaca mulatta
AB000554 Macaca mulatta
E29809 Novel IL-6
I27635 Sequence 3
I27637 Sequence 7
AF097333 Aotus lemniscatus
A57723 Sequence 1
A57726 Sequence 4
A57727 Sequence 5
A57728 Sequence 6
AR082464 Sequence
AR082467 Sequence
AR082468 Sequence
AR082469 Sequence
E02172 Human B cell
E02170 Human B cell
I52043 Sequence 19
I08634 Sequence 4
AF014510 Aotus nelsoni
S56892 Interleukin1h
A93806 Sequence 1
A93807 Sequence 2
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X04602 Human mRNA
A10873 pbSF2-L8 DN
A10875 pbSF2-L8 DN
A13367 pbSF2-L8 DN

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A68629	SEQUENCE	1 from Patent WO9803657.	DNA		
A68629	ACCESSION				
A68629.1	VERSION	G1:4759656			
	KEYWORDS	.			
ORGANISM	SOURCE	unidentified.			
REFERENCE	AUTHORS	unclassified.			
JOURNAL	TITLE	1 (bases 1 to 612)			
		Albrecht,J., Fleckenstein,B., Neipel,F., Friedman-Klen,A. and Huang,Y. VIRAL INTERLEUKIN-6 Patent: WO 9803657-A 1 29-JAN-1998; ALBRECHT JENS CHRISTIAN (DE) Location/Organism			
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ORIGIN					

Query Match	Similarity	100.0%	Score 612:	DB 9:	Length 612:
Best Local	Similarity	100.0%	Pred. No. 1,1e-175:		
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					Gaps 0:
QY 1	ATGTCGTGTTCAAGTTCCTGCTCTCTTGTGCGTGGTTCACCTGCTGTAATCGAAGC	60			
Db 1	ATGTCGTGTTCAAGTTCCTGCTCTCTTGTGCGTGGTTCACCTGCTGTAATCGAAGC	60			
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Db 61	CGGGCAAGTTCGCGGACGCCCGGAGTTTGAAAAGATCTTCTCATTCACAGACTCAAT	120			
QY 121	TGATGCTATGAGGTGATCGATGAATGCTTCGCGGACCTCTGTATACCGTACGGCATCGC	180			
Db 121	TGATGCTATGAGGTGATCGATGAATGCTTCGCGGACCTCTGTATACCGTACGGCATCGC	180			
QY 181	AAGGCTATTCAGAGCCCGCTGCTATTTTTCATCTGAAGATACAGCAGCATCAAGTACT	240			
Db 181	AAGGCTATTCAGAGCCCGCTGCTATTTTTCATCTGAAGATACAGCAGCATCAAGTACT	240			
QY 241	GATCCTCGGGGTTAATGAGATTAAATAGACTGCTGCTTAAAGCTGGCGGATGCG	300			
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Db 301	TTTTTGAATTCGAGGTGTGTTTAAAGTTTAAACGAGGAGTTTGAATAATCAGTGATA	360			
QY 361	AACGTGACGTCATGAGACTTCTGACGAAGACCTTAGATGGGACATACAGAGAGCTC	420			
Db 361	AACGTGACGTCATGAGACTTCTGACGAAGACCTTAGATGGGACATACAGAGAGCTC	420			
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Db 421	AATAAGCTAGTAAGACGCACTACAGTCCACCAATTTGACCGCGGCTATTAGAGAGG	480			
QY 481	CTTCAGGACTTAAGTATTTGGTGAGACACTTTGCTTGTATTTCTGATGTCAGTATG	540			
Db 481	CTTCAGGACTTAAGTATTTGGTGAGACACTTTGCTTGTATTTCTGATGTCAGTATG	540			
QY 541	GAAGAATTGAGGCAAGCGGCTGCTTTTGGACCTATCCAGACGATGCTGAC	600			
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Db 601	GTCACGATTAAG 612				
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LOCUS	KSU73655	612 bp	DNA	VRL	05-NOV-1996
DEFINITION	Kposi's sarcoma-associated herpes-like virus Interleukin-6 homolog (vIL-6) gene, partial cds.				
ACCESSION	U73655				
VERSION	U73655.1				
KEYWORDS	GI:1658011				
SOURCE	Kposi's sarcoma-associated herpesvirus - Human herpesvirus 8.				
ORGANISM	Human herpesvirus 8				
	Virus; dsDNA viruses, no RNA stage; Herpesviridae; Gammaherpesvirinae; Rhadinovirus.				
REFERENCE	1 (bases 1 to 612)				
AUTHORS	Neipel,F., Albrecht,J.-C., Essner,A., Huang,Y.-Q., Li,J.J., Friedman-Kien,A.-E. and Fleckenstein,B.				
TITLE	Human herpesvirus 8 encodes a homologue of Interleukin-6				
JOURNAL	J. Virol. (1996) In press				
REFERENCE	2 (bases 1 to 612)				
AUTHORS	Neipel,F., Albrecht,J.-C., Essner,A., Huang,Y.-Q., Li,J.J., Friedman-Kien,A.-E. and Fleckenstein,B.				
TITLE	Direct Submission				
JOURNAL	Submitted (08-OCT-1996) Institut fuer Klinische und Molekulare				

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Virologie, Universitaet Erlangen-Nuernberg, Schlossgarten 4,
Erlangen 91054, Germany
location/Qualifiers
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BASE COUNT 148 a 129 c 162 g 173 t
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Best Local Similarity 100.0%; Pred. No. 1,1e-175;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGTCGTTCAGTGTGCTCTCTCTGTCGTCACGTCGTCATCTGGAACG 60
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Db 601 GTCCAGATTAAG 612

RESULT 3
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LOCUS Sequence 1 from patent US 5861500.
DEFINITION
ACCESSION AR030968
VERSION AR030968.1 GI:5944182
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 615)
AUTHORS Chang,Y., Bohenzky,R.A., Russo,J.J., Edelman,I.S. and Moore,P.S.
TITLE Kaposi's sarcoma-associated herpesvirus (KSHV) Interleukin 6 (IL-6)
and uses thereof
Patent: US 5861500-A 1 19-JAN-1999;
JOURNAL Location/Qualifiers
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RESULT 4
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 DEFINITION Sequence 1 from patent US 5854398.
 ACCESSION AR069034
 VERSION AR069034.1 GI:6001241
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 615)
 AUTHORS Chang, Y., Bohenzky, R.A., Russo, J.J., Edelman, I.S. and Moore, P.S.
 TITLE Kaposi's sarcoma-associated herpesvirus (KSHV) Interleukin 6 (IL-6) and uses thereof
 JOURNAL Patent: US 5854398-A 1 29-DEC-1998;
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 source location/Qualifiers
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 BASE COUNT 150 a 129 c 162 g 174 t
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 Best Local Similarity 100.0%; Pred. No. 1..1e-175;
 Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTGCTGCTCAAGTGTGTCTCTCTCTGCTGCTGCTCACTGCTGATCTGGAGC 60
 DB 1 ATGTGCTGCTCAAGTGTGTCTCTCTCTGCTGCTGCTCACTGCTGATCTGGAGC 60
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 DB 61 CCGGGCAAGTGGCGGACCGCCCGGAGTTGAAAAGATCTCTCATTCAGACATCAAT 120
 QY 121 TCGATCTATGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 TCGATCTATGCTGATCATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 QY 181 AAGGATATCTAGAGCCCGCTGCTATTTTTCATCTGAACATACAGCATCAAGTACT 240
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 DB 541 GAAGAATTTGACAGGTCAAGCGGTGCTGTTTGGAGCTATATCCAGAGCTGACTCTGAC 600
 QY 601 GTCCAGATTAAG 612
 DB 601 GTCCAGATTAAG 612

RESULT 5

KSU67774
 LOCUS KSU67774 615 bp DNA VRL /28-JUN-1997
 DEFINITION Kaposi's sarcoma-associated herpes-like virus vIL-6 gene, complete cds.
 ACCESSION U67774
 VERSION U67774.1 GI:1562493
 KEYWORDS
 SOURCE Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8.
 ORGANISM Human herpesvirus 8
 REFERENCE 1 (bases 1 to 615)
 AUTHORS Nicholas, J., Ruvoilo, V., Zong, J., Clufo, D., Guo, H.G., Reitz, M.S. and Hayward, G.S.
 TITLE A single 13-kilobase divergent locus in the Kaposi's sarcoma-associated herpesvirus (human herpesvirus 8) genome contains nine open reading frames that are homologous to or related to cellular proteins
 JOURNAL J. Virol. 71 (3), 1963-1974 (1997)
 MEDLINE 97184526
 REFERENCE 2 (bases 1 to 615)
 AUTHORS Nicholas, J., Ruvoilo, V.R., Burns, W.H., Sandford, G., Man, X., Clufo, D., Hendrickson, S.B., Guo, H.G., Hayward, G.S. and Reitz, M.S.
 TITLE Kaposi's sarcoma-associated human herpesvirus-8 encodes homologues of macrophage inflammatory protein-1 and Interleukin-6
 JOURNAL Nat. Med. 3 (3), 287-292 (1997)
 MEDLINE 97208913
 REFERENCE 3 (bases 1 to 615)
 AUTHORS Nicholas, J.
 TITLE Direct Submission
 JOURNAL Submitted (22-AUG-1996) Johns Hopkins Oncology Center, 418 North Bond Street, Baltimore, MD 21231, USA
 FEATURES
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 Best Local Similarity 100.0%; Pred. No. 1..1e-175;
 Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 ATGTGCTGCTCAAGTGTGTCTCTCTCTGCTGCTGCTCACTGCTGATCTGGAGC 60
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QY 601 GTCCAGCATAG 612
Db 601 GTCCAGCATAG 612
RESULT 6
KSU71365/c 6600 bp DNA VRL 10-SEP-1998
LOCUS KSU71365
DEFINITION Kaposi's sarcoma-associated herpes-like virus fragment 1, putative
interleukin 6, dihydrofolate reductase and thymidylate synthase
genes, complete cds.
ACCESSION U71365
VERSION U71365.1 GI:3551754
KEYWORDS Kaposi's sarcoma-associated herpesvirus - Human herpesvirus 8.
SOURCE Human herpesvirus 8
ORGANISM Gammaherpesvirinae: Rhadinoviridae:
Viruses: dsDNA viruses, no RNA stage: Herpesviridae:
1 (bases 1 to 6600)
Sun, R., Lin, S.-F. and Miller, G.
Submitted (20-SEP-1996) Molecular Biophysics and Biochemistry, Yale
University School of Medicine, 333 Cedar Street, New Haven, Ct
06520, USA
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BASE COUNT 1697 a 1927 c 1536 g 1440 t
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Query Match 100.0%; Score 612; DB 59; Length 6600;
Best Local Similarity 100.0%; Pred. No. 1.7e-175;
Matches 612; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTCGCTGCTCAAGTGTGTCTCTCTGCTGGTTCACAGCTGATCTGGAACG 60
Db 2394 ATGTCGCTGCTCAAGTGTGTCTCTCTGCTGGTTCACAGCTGATCTGGAACG 2395
QY 61 CGGGCAAGTTGCGGAGCGCCCGAGTTGAAAAGATCTTCATTCACAGACTCAAT 120
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Db 2274 TGAATGCTATGAGGATGATGATGCTTCGCGACCTCTGTTACCGTACCGGATCTGC 2215
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Db 2214 AAGGTAATTCAGAGCCCGCTATTTTCATCTGAAACATCAGCAGCATCAAGCATCT 2155

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Db 2094 TTTTGGAAATTCAGAGTGTGTTAGTTTAAAGACAGAGAGTTTGGAAATACAGATA 2035
OY 361 AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGGAGACATACAGAAAGACTC 420
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Db 2034 AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGGAGACATACAGAAAGACTC 1975
OY 421 AATAAGCTACTAAGACGACACTACACTCCACCAGAAATTTGACCGCGCTATTAGGAGG 480
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Db 1974 AATAAGCTACTAAGACGACACTACACTCCACCAGAAATTTGACCGCGCTATTAGGAGG 1915
OY 481 CTTCAGGACTTAAGATTATGGGTGAGACACTTTGCTTGTATTATGTCGATGCAATG 540
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Db 1794 GTCCACGATTAAG 1783

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RESULT 7
AR065849/c 35100 bp DNA PAT 29-SEP-1999
LOCUS AR065849
DEFINITION Sequence 17 from patent US 5849564.
ACCESSION AR065849
VERSION AR065849.1 GI:5996065
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 35100)
AUTHORS Chang,Y., Hohenzky,R.A., Russo,J.J., Edelman,I.S. and Moore,P.S.
TITLE Polypeptides from Kaposi's sarcoma-associated herpesvirus, DNA
JOURNAL Patent: US 5849564-A 17 15-DEC-1998;
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source location/Qualifiers
1..35100
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BASE COUNT 8703 a 9395 c 8921 g 8081 t
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Best Local Similarity 100.0%; Pred. No. 2,4e-175;
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OY 121 TGGATCTATGAGTGCATGATGATGATCTTCGCGACCTCTGTTACCGTACCGGATCTGC 180
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Db 17755 TGGATCTATGAGTGCATGATGATGATCTTCGCGACCTCTGTTACCGTACCGGATCTGC 17696
OY 181 AAGGATATTCAGAGCCCGCTGCTATTTTTCATCTGAAACTACACAGCATCAACGATCT 240
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OY 361 AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGGAGACATACAGAAAGACTC 420
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Db 17515 AACGTGAGCTCATGAGCTTCTGACGAAGACCTTAGATGGAGACATACAGAAAGACTC 17456
OY 421 AATAAGCTACTAAGACGACACTACACTCCACCAGAAATTTGACCGCGCTATTAGGAGG 480
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Db 17275 GTCCACGATTAAG 17264

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RESULT 8
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LOCUS KSU75698
DEFINITION Kaposi's sarcoma-associated herpesvirus long unique region, 80
ACCESSION KSU75698
VERSION KSU75698.1 GI:2065526
KEYWORDS
SOURCE Human herpesvirus 8.
ORGANISM Human herpesvirus 8.
REFERENCE 1 (bases 47193 to 47522; 133099 to 133729)
AUTHORS Chang,Y., Cesarman,E., Pessin,M.S., Lee,F., Culpepper,J.,
TITLE Identification of herpesvirus-like DNA sequences in AIDS-associated
JOURNAL Kaposi's sarcoma
Science 266 (5192), 1865-1869 (1994)
95090463
JOURNAL 2 (bases 35021 to 55726)
MEDLINE Moore,P.S., Gao,S.J., Dominguez,G., Cesarman,E., Lungu,O.,
AUTHORS Knowles,D.M., Gardner,R., Pellet,P.E., McGeoch,D.J. and Chang,Y.
TITLE Primary characterization of a herpesvirus agent associated with
JOURNAL Kaposi's sarcoma
J. Virol. 70 (1), 549-558 (1996)
96099469
JOURNAL 3 (bases 28661 to 29741; 117919 to 118101)
MEDLINE Zhong,W., Wang,H., Herndler,B. and Ganem,D.
AUTHORS Restricted expression of Kaposi sarcoma-associated herpesvirus
JOURNAL (human herpesvirus 8) genes in Kaposi sarcoma
Proc. Natl. Acad. Sci. U.S.A. 93 (13), 6641-6646 (1996)
96270595
JOURNAL 4 (bases 122794 to 123567; 123809 to 127297; 129372 to 130400;
MEDLINE 130551 to 134441)
AUTHORS Cesarman,E., Nador,R.G., Bai,F., Hohenzky,R.A., Russo,J.J.,
TITLE Moore,P.S., Chang,Y. and Knowles,D.M.
JOURNAL Kaposi's sarcoma-associated herpesvirus contains G protein-coupled
AUTHORS receptor and cyclin D homologs which are expressed in Kaposi's
TITLE sarcoma and malignant lymphoma
J. Virol. 70 (11), 8218-8223 (1996)
97048116
JOURNAL 5 (bases 1 to 137508)
MEDLINE Moore,P.S., Boshoff,C., Weiss,R.A. and Chang,Y.
AUTHORS Molecular mimicry of human cytokine and cytokine response pathway
TITLE genes by KSHV

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JOURNAL Science 274 (5293), 1739-1744 (1996)
 MEDLINE 97094384
 REFERENCE 6 (bases 1 to 137508)
 AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M.,
 Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and
 Moore,P.S.

TITLE Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus
 (HHV8)
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (25), 14862-14867 (1996)
 MEDLINE 97121480
 REFERENCE 7 (bases 1 to 137508)
 AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M.,
 Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and
 Moore,P.S.

TITLE Direct Submission
 JOURNAL Submitted (17-OCT-1996) Dept of Pathology/Genome Center/Division of
 Epidemiology, Columbia University, 650 West 168th Street, New York,
 NY 10032, USA
 REFERENCE 8 (bases 1 to 137508)
 AUTHORS Russo,J.J., Bohenzky,R.A., Chien,M.-C., Chen,J., Yan,M.,
 Maddalena,D., Parry,J.P., Peruzzi,D., Edelman,I.S., Chang,Y. and
 Moore,P.S.

TITLE Direct Submission
 JOURNAL Submitted (02-MAY-1997) Dept of Pathology/Genome Center/Division of
 Epidemiology, Columbia University, 650 West 168th Street, New York,
 NY 10032, USA

REMARK Sequence update by submitter
 COMMENT On May 3, 1997 this sequence version replaced gi:1718251.
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 U75700. The remaining LUR sequence extending from this
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 105..974
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 1142..2794
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 homolog"
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 DB 17376 CTTTACGAGCTCATGAGCTTCTGACGAAGACCTTAGATGGACATACAGGAAGAGCTC 17317
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RESULT 10
 LOCUS A57729 555 bp DNA PAT 03-MAR-1998
 DEFINITION Sequence 7 from Patent WO9634104.
 ACCESSION A57729
 VERSION A57729.1 GI:3713553
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unclassified.
 REFERENCE 1 (bases 1 to 555)
 AUTHORS Cliberto, G., Savino, R. and Ponessa, G.
 TITLE ANTAGONISTS OF HUMAN INTERLEUKIN-6 THAT ARE TOTALLY INCAPABLE OF BINDING GP 130, AND THEIR USE IN THE PREPARATION OF PHARMACEUTICAL COMPOUNDS
 JOURNAL Patent: NO 9634104-A 7 31-OCT-1996;
 FEATURES
 SOURCE 1..555
 /organism="unclassified"
 /db_xref="taxon:32644"
 Location/Qualifiers
 BASE COUNT 178 a 140 c 130 g 107 t
 ORIGIN

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 Matches 184; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 160 TGTTCACCGTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 219
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 QY 220 CTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 279
 DB 190 CTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 249
 QY 280 CTTTAAAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 339
 DB 250 CTTTAAAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 309
 QY 340 GACTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 399
 DB 310 GACTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 369
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 DB 370 TGGGACATACAGGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 429
 QY 460 GACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 519
 DB 430 GACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 489

QY 520 TTTATGTTCTGAGCTCATGAGGATTT 548
 DB 490 CATCTATCTTCTGAGCTCATGAGGATTT 518

RESULT 11
 LOCUS AR082470 555 bp DNA PAT 31-AUG-2000
 DEFINITION Sequence 7 from patent US 5972902.
 ACCESSION AR082470
 VERSION AR082470.1 GI:10009196
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 555)
 AUTHORS Cliberto, G., Savino, R. and Ponessa, G.
 TITLE DNA encoding human IL-6 receptor antagonist and protein encoded thereby
 JOURNAL Patent: US 5972902-A 7 26-OCT-1999;
 FEATURES
 SOURCE 1..555
 /organism="unknown"
 Location/Qualifiers
 BASE COUNT 178 a 140 c 130 g 107 t
 ORIGIN

Query Match 10.0%; Score 61; DB 9; Length 555;
 Best Local Similarity 47.3%; Pred. No. 1.4e-07;
 Matches 184; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 160 TGTTCACCGTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 219
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 DB 190 CTACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 249
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 QY 340 GACTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 399
 DB 310 GACTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 369
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 DB 370 TGGGACATACAGGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAGAGCTTTCAG 429
 QY 460 GACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 519
 DB 430 GACCGGATCTGCAAGGATTTCTAGAGCCCGCTGATTTTTCATCTGAAA 489

RESULT 12
 LOCUS CEYIN6A 639 bp mRNA PRI 16-MAY-1996
 DEFINITION Cercopithecus torquatus Interleukin 6 mRNA, complete cds.
 ACCESSION L26032
 VERSION L26032.1 GI:514341
 KEYWORDS
 SOURCE Interleukin 6.
 ORGANISM Cercopithecus torquatus (Individual isolate FUJ) cDNA to mRNA.
 Cercopithecus torquatus
 Eukaryota; Metazoa; Chordata; Gratiata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Cercopithecus.

Query Match 8.9%; Score 54.6; DB 9; Length 555;
 Best Local Similarity 46.3%; Pred. No. 1.2e-05;
 Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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RESULT 15
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 LOCUS AR021247 555 bp DNA
 DEFINITION Sequence 1 from patent US 5789552. PAT 05-DEC-1998
 ACCESSION AR021247
 VERSION AR021247.1 GI:3975862
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 555)
 AUTHORS Savino, R., Lamm, A. and Ciliberto, G.
 TITLE Interleukin-6 receptor antagonists
 JOURNAL Patent: US 5789552-A 1 04-AUG-1998;
 FEATURES Location/Qualifiers
 source 1..555
 ORIGIN /organism="unknown"
 BASE COUNT 183 a 136 c 129 g 107 t

Query Match 8.9%; Score 54.6; DB 9; Length 555;
 Best Local Similarity 46.3%; Pred. No. 1.2e-05;

Matches 180; Conservative 0; Mismatches 209; Indels 0; Gaps 0;

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Title: US-09-230-048-1

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Scoring table: IDENTITY NUC
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Searched: 10228115 seqs, 4726426750 residues

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Post-processing: Minimum Match 0%

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Listing first 45 summaries

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SUMMARIES

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C 8	42	6.9	898	140	BE798809	BE798809
C 9	41.8	6.8	898	140	BE798809	BE798809
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C 11	40.8	6.7	1101	219	BE866701	BE866701
C 12	40.2	6.6	689	250	AN2829745	AN2829745
C 13	39.2	6.4	313	26	AV2074422	AV2074422
C 14	38.8	6.3	1101	219	CNS00370	CNS00370
C 15	38.6	6.3	266	6	AA388057	AA388057
C 16	38.6	6.3	326	25	AV139780	AV139780
C 17	38.2	6.2	280	6	AA381568	AA381568
C 18	38.2	6.2	305	109	AV087294	AV087294
C 19	38.2	6.2	481	24	AT751501	AT751501
C 20	38.2	6.2	517	118	AM630744	AM630744
C 21	38.2	6.2	860	219	CNS018FL	CNS018FL
C 22	38.2	6.2	863	106	AL544265	AL544265
C 23	38.2	6.2	924	140	BE789477	BE789477
C 24	38	6.2	292	126	BB112636	BB112636
C 25	37.2	6.1	289	133	BB411023	BB411023
C 26	37.2	6.1	302	26	AV220080	AV220080
C 27	37.2	6.1	468	228	AC452435	AC452435
C 28	37	6.0	293	35	AV136471	AV136471
C 29	36.8	6.0	264	9	AA606518	AA606518
C 30	36.8	6.0	334	108	AV019824	AV019824
C 31	36.8	6.0	557	12	AA792350	AA792350
C 32	36.6	6.0	282	25	AV161042	AV161042
C 33	36.6	6.0	613	156	C88575	C88575
C 34	36.4	5.9	277	109	AV079167	AV079167
C 35	36.4	5.9	295	25	AV170382	AV170382
C 36	36.4	5.9	431	26	AV213586	AV213586
C 37	36.4	5.9	455	225	AN225616	AN225616
C 38	36.2	5.9	293	109	AV040844	AV040844
C 39	36	5.9	281	109	AV075319	AV075319
C 40	36	5.9	322	25	AV105835	AV105835
C 41	35.6	5.8	281	28	AV266533	AV266533
C 42	35.6	5.8	282	109	AV068892	AV068892
C 43	35.4	5.8	272	109	AV095645	AV095645
C 44	35.4	5.8	282	109	AV035279	AV035279
C 45	35.4	5.8	284	25	AV120780	AV120780

ALIGNMENTS

[illegible]

[illegible]

VERSION BE439832.1 GI:9439443
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 600)
 AUTHORS Gonzalez,P., Epstein,D.L. and Borras,T.
 TITLE Characterization of gene expression in human trabecular meshwork
 using single-pass sequencing of 1060 clones
 Invest. Ophthalmol. Vis. Sci. (2000) In press
 JOURNAL Contact: Pedro Gonzalez
 Department of Ophthalmology
 Duke University
 Duke Eye Center, Erwin Rd, Box 3802, Durham, NC 27710-3802, USA
 Tel: 919 681 4085
 Fax: 919 684 8983
 Email: pedro.gonzalez@duke.edu,
 location@qualifiers
 FEATURES
 source 1..600
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="HM1"
 /lssue_type="Trabecular meshwork"
 BASE COUNT 182 a 112 c 131 g 173 t 2 others
 ORIGIN
 Query Match 7.0% Score 43; DB 167; Length 600;
 Best Local Similarity 46.5%; Pred.NO. 0.019; Indels 0; Gaps 0;
 Matches 139; Conservative 0; Mismatches 160; Indels 0; Gaps 0;
 QY 235 GATACGTACATCGGGGTTAATAGATTTAATGAAGACTCTGTAAAGTCGCC 294
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 2 GAATAAGTATGATGCCTCCATCATCTGATTCATCAAGAGCGACTTGTAAGAATC 61
 QY 295 CATGCTTTTTGAATTCGAGCTGTCTTTTAACTTTTAAACAGGACTTTGAAAAATCA 354
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 62 ACTGCTCTTTGGAGTTTAGAGTATACCTAGAGTACCCTCCGAACAAGATTGGAAGTAGT 121
 QY 355 GTGATAAACGTGGAGCTCATGAGCTTCTTGACGAAGACCTTAGGATGGACATACAGAA 414
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 122 GAGGACAAAGCCAGAGCGTGTGACAGTAGATCAAAGATCCATGATCCAGTTCTGCAGAAA 181
 QY 415 GAGCTCAATTAAGCTGACTAAGACGACACTACAGTCCACCCAATTGACCGCGGTCTATTA 474
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 182 AAGCCAAAGATCTAGATGCAATTAACACCCCCCTGACCCMACCAAAATGCCACGCTCTG 241
 QY 475 GGAGAGCTTCAGGACCTTAATGTTGGTGGAGACACTTTCCTTGCTTTATGTTCTGAG 533
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 242 ACGAAGCTGCAGGCACAGAACCACTGGTGGCAGGACATGACACTCATCTTCATTTCTGG 300
 RESULT 8
 LOCUS BE789809 mRNA EST 20-OCT-2000
 DEFINITION 601481651F1 NIH_MGC_68 Homo sapiens cdna clone IMAGE:3884173 5',
 mrna sequence.
 ACCESSION BE789809
 VERSION BE789809.1 GI:10211007
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euarchonta; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 898)
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: gcgabs@email.nih.gov
 Tissue Procurement: DCTD/DTP/Gazdar
 CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM9657 row: f column: 14
 High quality sequence stop: 734.

FEATURES

source

1. 698
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3884173"
 /clone_lib="NIH_MGC_68"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pCMV-Sport6; Site.1: NotI;
 Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.8 kb. Library constructed by Life
 Technologies."
 BASE COUNT 269 a 150 c 217 g 262 t
 ORIGIN

Query Match 6.8%; Score 42; DB 140; Length 898;
 Best Local Similarity 46.6%; Pred. No. 0.044;
 Matches 135; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

OY 259 GGATTTAAGAGACTAGCTCCCTTAAAGCTGGCCGATGCTTTTGAATCGAGTG 318
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 5 GGATTCATAGAGAGACTCCCTGGTGAATATCATCTGCTCTTGGAGTTGAGGTA 64
 OY 319 TTGTTTAAGTTTAAAGCAGGAGTTTGAATACAGTGAATACGTGACGTGATGAG 378
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 65 TACCTAGAGTACCTCCAGAACAGATTGAGAGTAGTAGAGAACAGCCAGCTGTCCAG 124
 OY 379 CTCTGACAGACCTTGAAGTGGACATACAGAGAGAGCTCAATAAGCTGACTAAGACG 438
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 125 ATGAGTACAAAAGTCCGTGATCCAGTTCCTGAGAAAAGGCAAGAACTAGATGCATA 184
 OY 439 CACTACAGTCCAGCAAAATTTGACCCGGGTCATTAGGAGGCTTCAGGACTTAAGTAT 498
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 185 ACCACCCCTACACCAACCAAAATGCCAGCTGCTGACGAAAGCTGACAGAACCG 244
 OY 499 TGGGTGAGACACTTGGCTTGTATGTTCTGAGTCAATGAAAAATT 548
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 245 TGGGTGAGAGACATGACACTCATCTTCCTGCCAGCTTTAAGAGATT 294

RESULT

9

AM637075 617 bp mRNA EST 03-APR-2000
 LOCUS b154a09.w1 Blackshear/Soares normalized Xenopus egg library Xenopus
 DEFINITION laevis cDNA clone PBX0054A09 5', mRNA sequence.

ACCESSION AM637075
 VERSION AM637075.1 GI:7394175
 KEYWORDS EST.
 SOURCE African clawed frog.
 ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 617)
 AUTHORS Blackshear,P.J., Lai,W.S., Thorn,J.M., Kennington,E.A., Stafla,N.G.,
 Jr., Moore,D.T., Bouffard,G.G., Beckstrom-Sternberg,S.M., Touchman
 J.W., Bonaldo,M.F. and Soares,M.B.
 The NIH's Xenopus Maternal EST Project
 Unpublished (2000)
 CONTACT: Perry J. Blackshear
 Office of Clinical Research and Laboratory of Signal Transduction
 National Institute of Environmental Health Sciences
 A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
 USA
 Tel: 919 541-4899

Fax: 919 541-4571
 Email: black009niehs.nih.gov
 Clone is available through Research Genetics, Inc., 2130 Memorial
 Parkway, Huntsville, AL 35901
 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
 cdnaeresgen.com

DNA Sequencing and analyses performed by National Institutes of
 Health Intramural Sequencing Center (NISC).

PCR Primers

FORWARD: TGTAAACGACGGCCAGT

BACKWARD: CAGCAACACGCTATGACC

Plate: 0054 row: A column: 09

Seq primer: 17 primer.

Location/Qualifiers

1. 617

/organism="Xenopus laevis"

/db_xref="taxon:8355"

/clone="PBX0054A09"

/clone_lib="Blackshear/Soares normalized Xenopus egg
 library"

/sex="female"

/tissue_type="unfertilized egg"

/cell_type="unfertilized egg"

/dev_stage="unfertilized egg"

/lab_host="DH10B"

/note="Vector: pT73-Pac; Site.1: EcoRI; Site.2: NotI;
 PolyA-selected mRNA was prepared from unfertilized Xenopus
 laevis eggs. The library was constructed in the vector
 pT73-Pac as described in Bonaldo, M.F., Lennon, G. and
 Soares, M.B. 'Normalization and subcloning: two
 approaches to facilitate gene discovery', Genome Research
 6:791-806, 1996. The first strand synthesis used a
 NotI-dT18 primer; double stranded cDNAs were ligated to
 EcoRI adapters, digested with NotI, and directionally
 cloned into the NotI and EcoRI-digested pT73-Pac vector.
 The library contained approximately 7.2 x 10⁵
 recombinants, with average insert sizes of 1-1.5 kb."

BASE COUNT

220 a 109 c 110 g 178 t

ORIGIN

Query Match 6.8%; Score 41.8; DB 118; Length 617;
 Best Local Similarity 49.8%; Pred. No. 0.046;
 Matches 106; Conservative 0; Mismatches 107; Indels 0; Gaps 0;

OY 212 ATCTGAACATACAGCCATACAGTATCATCTCCGGTTAATGATTAATAGA 271
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 DB 29 ACCTGACGCTCCCTAAATAACCACTAAGATAGCTCTTCTCTGAGATTCCAAAAGA 88
 OY 272 CTAGCTGCTTAAAGCTGCGCATGCTTTTGAATCGAGTGTGTTAAGTTT 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 89 ACAATGCCGTGAATTAATATCCACGACGACTGTGATATTTGAGATCTACTGATG 148
 OY 332 TAAAGGAGAGTTTGAATAATCACTGATTAACGTGACGTATGAGACTTCTGACGAGA 391
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 149 TGAAGGAGACTTTCAGAAAGTGAAGAAGCACTTGGAGTCATGATTAACAAGCAATG 208
 OY 392 CCTTAGATGGGACATACAGAAAGAGCTCAATA 424
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 DB 209 TATTAAAGGGGCCATTAAAGAGATGATGAAA 241

RESULT

10

BE786701 649 bp mRNA EST 20-OCT-2000
 LOCUS 601475036F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3878244 5',
 DEFINITION mRNA sequence.

ACCESSION BE786701
 VERSION BE786701.1 GI:10207899
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

RESULT 14	CNS00370	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
	CNS00370	1101 bp	DNA	GSS	03-JUN-1999							
			Drosophila melanogaster genome survey sequence TERN3 end of BAC #									
			BACR08B14 of Rp11-98 library from Drosophila melanogaster (fruit									
			fly), genomic survey sequence.									
				AL064465								
				AL064465.1	GI:4941722							
				GSS.								
				fruit fly.								
				Drosophila melanogaster								
				Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;								
				Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;								
				Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.								
				1 (bases 1 to 1101)								
				Genoscope.								
				Direct Submission								
				Submitted (03-JUN-1999)								
				Genoscope - Centre National de Sequencage								

BASE COUNT	ORIGIN	FEATURES	SOURCE	COMMENT	
374 a	61 c	78 g	129 t	459 others	<p>JOURNAL</p> <p>Submitted (02-JUN-1999) Genoscope - Centre National de Séquençage BP 191 91006 EVRY cedex - FRANCE (E-mail : seq@genoscope.cns.fr - Web : www.genoscope.cns.fr)</p> <p>Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the <i>Drosophila melanogaster</i> genome using these BACs. For further information please see http://www.fruitfly.org The BDGP <i>Drosophila melanogaster</i> BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial <i>ECORI</i> digestion of <i>Drosophila</i> DNA provided by the BDGP from the isogenic strain Y2: cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.</p> <p>Location/Qualifiers</p> <p>1..1101</p> <p>/organism="Drosophila melanogaster"</p> <p>/db_xref="taxon:7227"</p> <p>/clone_1lb="RPCI-98"</p> <p>/clone="BAC08K14"</p> <p>/note="end : TET3"</p>

	Query Match	6.3%	Score 38.8;	DB 219;	Length 1101;
	Best Local Similarity	17.7%	Pred. No. 0.47;		
	Matches	45;	Conservative 103;	Mismatches 106;	Indels 0; Gaps 0;
OY	348	AAATCATGATTAACCGTCGCAGCTGTATGGAGCTTTCGACAGAAGACCTTTAGCATGGACAT	407		
Dh	721	TAGAMATTATATAAATAARAKKKNKKRGTKATDCKDKMGKGMWHKKRKKDDKKMKGAAT	780		

RESULT	15
AA388057/c	
LOCUS	
DEFINITION	AA388057.1 266 bp mRNA EST 23-APR-1997
ACCESSION	U886C08.11 KO mouse embryo 11 5dpc Mus musculus cDNA clone
IMAGE	IMAGE:7899902.5 similar to gb:225749_1nal 40S RIBOSOMAL PROTEIN S7 (HUMAN);, mRNA sequence.
AA388057	
KEYWORDS	AA388057.1 GI:2041073
VERSION	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus
AUTHORS	1 (pages 1 to 265)
	Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geiselt,S., Kucaba,T., Jacy,M., Le,M., Martin,D., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
TITLE	The WashU-HMI Mouse EST project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST project WashU-HMI Mouse EST project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.wustl.edu This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:474310
FEATURES	Trace considered overall poor quality High quality sequence stop: 1. Location/Qualifiers

```

FEATURES
SOURCE
    Location/Qualifiers
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    /strain="C57BL/6J"
    /db_xref="taxon:10090"
    /clone_image="789902"
    /clone_id="No mouse embryo 11 5dpc"
    /sex="pooled"
    /tissue_type="embryo"
    /dev_stage="11.5dpc"
    /lab_host="DH10B"
    /note="Organ: embryo; Vector: pSPORT1; Site_1: SalI;
    Site_2: NotI; total RNAs were extracted from 11.5 dpc
    embryos (excluding placenta and yolk sac). The
    double-stranded cDNA was synthesized with an oligo (dN)-1
    primer gagagagacactgacttcttgatgcggagcgccgtttttttttttt
    3'. The cDNAs were ligated to L1-Sal3a: 5'
    gctattgacgtgcacatcttc 3' and L1-Sal3b: 5'
    ggatnctgcagctccaat 3'. The cDNAs were size-selected and
    amplified by long-range PCR using Ex Taq polymerase for 18
    cycles. The PCR-amplifiable cDNA mixture went through
    one round of equalization and was digested with SalI/NotI
    and cloned into the SalI/NotI sites of the pSPORT1

```


Fri, Oct 5 10:02:06 2001

us-09-230-048-1.rst

Page 11

BASE COUNT 97 a 49 c 59 g 61 t
ORIGIN Wangⁿ

Query Match	6.38;	Score 38.6;	DB 6;	Length 266;
Best local Similarity	58.18;	Pred. No. 0.37;		
Matches 68;	Conservative 0;	Mismatches 49;	Indels 0;	Gaps 0;

QY 72 GCCGGAGCCCCCAGTTTAAAGAACTCTCATTCACAGAGCATCAATGGATGCTATG 131
 120 GCCGGCTCCATCCAGTTTACATGATGATCCCTTATCCACAAATTCACCTTGGAGACTA 61
 QY 132 GGTATCGATCAAAAGCTTCCCGGACACTCTGTACCCGACCGGATCTGCAAGGTAA 188
 Db 60 AGTCTCAAGATGTCTGTCGACACTTGTGTAGGTACTGTCTTTCGGAAAGATT 4

Search completed: October 4, 2001, 17:36:01
Job time: 5107 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 4, 2001, 18:24:14 ; Search time 54.44 Seconds
(without alignments)
227.173 Million cell updates/sec

Title: US-09-230-048-2
Perfect score: 1095
Sequence: 1 MCFRLMSLLVGSLLVSGT.....GQAVRVLDSPDVPVHDR 204

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_0601:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
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- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
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- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDSL/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1095	100.0	204	19	AAW74570
2	1095	100.0	204	19	AAW40103
3	1095	100.0	204	19	AAW23944
4	992	90.6	185	20	AAW95015
5	188	17.2	184	17	AAW02611
6	187	17.1	184	17	AAW02611
7	185.5	16.9	184	17	AAW08477
8	184.5	16.8	184	17	AAW08476
9	184	16.8	201	9	AAW81162
10	183.5	16.8	184	17	AAW07200
11	183.5	16.8	184	19	AAW58519

12	183.5	16.8	184	20	AAW92803	Human IL-16 mutein
13	183.5	16.8	500	18	AAW36847	Human fusion polyp
14	183.5	16.8	525	18	AAW36846	Human fusion polyp
15	183	16.7	169	16	AAW7387	Human IL-6 mutant
16	183	16.7	185	15	AAW45720	Full length Interl
17	183	16.7	185	15	AAW45718	Full length Interl
18	183	16.7	211	13	AAW25279	Mutant human BCDP
19	183	16.7	212	8	AAW70238	Interferon-beta 2a
20	183	16.7	212	9	AAW80269	Recombinant Interl
21	183	16.7	212	10	AAW90047	pBSF2-18 sequence
22	183	16.7	212	10	AAW90371	pBSF2-18. AAP903
23	183	16.7	212	10	AAW90436	Interferon-beta-2.
24	183	16.7	212	10	AAW90469	Interleukin-6. Ho
25	183	16.7	212	11	AAW05415	Human B-cell diffe
26	183	16.7	212	14	AAW3430	IFN-beta-2a. Homo
27	183	16.7	212	14	AAW34726	Human IL-6 (for mo
28	183	16.7	212	15	AAW49041	Human Interleukin-
29	183	16.7	212	15	AAW49249	Sequence of human
30	183	16.7	212	16	AAW72317	Human Interleukin-
31	183	16.7	212	18	AAW35878	Human Interleukin-
32	183	16.7	212	18	AAW33643	Human Interleukin-
33	183	16.7	212	21	AAW87816	Human IL-6 protein
34	182	16.6	185	18	AAW13999	Interleukin-6 rece
35	181	16.5	179	16	AAW73534	Human Interleukin-
36	181	16.5	183	15	AAW60125	Human Interleukin-
37	181	16.5	184	9	AAW81158	Sequence of varian
38	181	16.5	184	10	AAW94753	Polypeptide with B
39	181	16.5	184	11	AAW05532	Human B-cell stiml
40	181	16.5	184	11	AAW03914	Interleukin-6. A
41	181	16.5	184	13	AAW20783	Polypeptide with h
42	181	16.5	184	15	AAW54990	Mutant Interleukin
43	181	16.5	184	15	AAW55256	Interleukin 6. Ho
44	181	16.5	184	16	AAW74659	Interleukin-6 for
45	181	16.5	184	16	AAW68623	B-cell differentia

ALIGNMENTS

RESULT	1
ID	AAW74570 standard; Protein: 204 AA.
AC	AAW74570;
XX	XX
DT	04-DEC-1998 (first entry)
XX	XX
DE	Kaposi sarcoma herpes-like virus/Interleukin-6.
XX	XX
KW	Kaposi sarcoma herpes-like virus/Interleukin-6; PCR primer;
KW	antiviral agent; multiple myeloma; vaccine; rheumatoid arthritis;
KW	monoclonal gammopathy of undetermined significance; MGUS; malignant;
KW	Interleukin-6; Alzheimer's disease; multiple sclerosis; scleroderma;
KW	systemic lupus erythematosus; amplification.
XX	XX
OS	Synthetic.
XX	XX
PN	W09835684-A2.
XX	XX
PD	20-AUG-1998.
XX	XX
PF	12-FEB-1998; 98WO-US02820.
XX	XX
PR	11-NOV-1997; 97US-0967504.
PR	14-FEB-1997; 97US-0800710.
XX	XX
PA	(BERE/) BERENSON J R.
PA	(RETT/) RETTING M B.
PA	(VESC/) VESCIO R A.
XX	XX
PI	Berenson JR, Rettig MB, Vescio RA;
XX	XX
DR	WPI; 1998-480765/41.

DR N-PSDB: AAV54070.
 XX Treatment of multiple myeloma and monoclonal myopathy with antiviral
 PT agent - active against Kaposi sarcoma virus, or with inhibitory
 PT nucleic acid or antibody against this virus
 XX
 PS Disclosure: Fig 5b: 137pp: English.
 XX
 CC This is the amino acid sequence of the Kaposi sarcoma herpes-like
 CC virus/interleukin-6, used in the method of the invention. In this
 CC method, an antiviral agent effective against Kaposi sarcoma
 CC herpes-like virus (KSHV), is used to prevent progression of MGUS to
 CC multiple myeloma or related malignancy. KSHV- and/or Interleukin-6
 CC related disorders such as specifically Alzheimer's disease, multiple
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus,
 CC scleroderma and malignancies of kidney or head/neck. The vaccines
 CC (comprising a KSHV-specific immunogen) is used to produce a
 CC therapeutic and/or prophylactic response.
 CC
 SQ Sequence 204 AA:

Query Match 100.0%: Score 1095; DB 19; Length 204;
 Best Local Similarity 100.0%: Pred. No. 2,7e-118;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCFKMLSLVLSGSLVSGTRGKLPDAPFEKDLIQLRNLMLWYDECFRDLCTRTGIC 60
 DB 1 mcfkmlslvlsvglsvstrgklpdapefekdlilqlrnlmlwvdecfldlcyrtgic 60
 OY 61 KGLLEPAAIFHLKLPAINDTDHGCLIGFNETSCLKKIADGFEFEVLPKFLTTEFGKSVI 120
 DB 61 kgllepaaifhlklpaindthcgligfnetacikkladgffefevlpkflttefgksvi 120
 OY 121 NYDVMEILTKTLGMDIOEELNLTGTHYSPKFDGCLGRLOGLKYYWVHFAFVLSM 180
 DB 121 nydvmeilctklgwdlgeelnltcthyppkfdrgligriglkyywvthasfvlasm 180
 OY 181 EKFAQAVRVLDSPDVPDVHDK 204
 DB 181 ekfaqavrvldslpdpvindhk 204

RESULT 2

ID AAW40103 standard; Protein; 204 AA.

XX AAW40103;

DT 15-JUL-1998 (first entry)

DE Human herpesvirus 8 (HHV-8) Interleukin-6.

XX DL-B; thymidylate synthase; dihydrofolate reductase; primer: HHV-8;
 KW Bcl-2 homologue; IE-1A; IE-1B; viral macrophage inhibitory protein;
 KW Kaposi's sarcoma; beta-chemokine-like; amplification; PCR; VIL-6.
 XX Kaposi's sarcoma associated herpesvirus.
 OS

PN WO9804284-A1.

PD 05-FEB-1998.

PF 24-JUL-1997; 97WO-US12931.

PR 25-JUL-1996; 96US-0022591.

PA (UJJO) UNITV JOHNS HOPKINS.

PI Hardwick JM, Hayward GS, Nicholas J, Reitz MR;

DR WPI; 1998-130422/12.

PT New human herpes virus gene region containing 8 open reading frames
 PT - useful for, e.g., diagnosing Kaposi's sarcoma or body cavity based
 PT large cell lymphoma
 XX
 PS Claim 1: Pages 59-60; 84pp: English.

XX The sequence represents a novel human herpesvirus 8 (HHV-8)
 CC Interleukin-6. The invention claims for novel genes, which includes
 CC the viral interleukin-6 gene, found at the divergent DL-B locus. HHV-8
 CC divergent locus DL-B lies between open reading frames 11 and 17.
 CC Sequencing of the HHV-8 divergent locus DL-B revealed the presence of
 CC nine viral ORFs with gene products related to cellular proteins. These
 CC proteins include the thymidylate synthase (TS, AAW40100), dihydrofolate
 CC reductase (DHFR, see AAW40101), Bcl-2 homologue (AAW40102), IE-1A
 CC (AAW40107), IE-1B (AAW40108) and, four cytokines which include viral
 CC interleukin-6 (vIL-6), viral macrophage inhibitory protein (vMIP)-1A
 CC (AAW40104) and -1B (AAW40105) and beta-chemokine-like (BCK, AAW40106)
 CC protein. The invention claims the mentioned proteins and a
 CC polynucleotide containing HHV-8 genes encoding one or more of these
 CC proteins. The invention also claims that the polynucleotide and the
 CC proteins may be used directly or indirectly, e.g. using antibodies to the
 CC proteins, to diagnose an HHV-8 associated disease, e.g. Kaposi's sarcoma,
 CC Castleman's disease, multiple myeloma and body cavity based large cell
 CC lymphoma (BCBL). The proteins have also been claimed to be useful in
 CC screening compounds for drugs to treat HHV-8 diseases.
 CC
 SQ Sequence 204 AA:

Query Match 100.0%: Score 1095; DB 19; Length 204;
 Best Local Similarity 100.0%: Pred. No. 2,7e-118;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCFKMLSLVLSGSLVSGTRGKLPDAPFEKDLIQLRNLMLWYDECFRDLCTRTGIC 60
 DB 1 mcfkmlslvlsvglsvstrgklpdapefekdlilqlrnlmlwvdecfldlcyrtgic 60
 OY 61 KGLLEPAAIFHLKLPAINDTDHGCLIGFNETSCLKKIADGFEFEVLPKFLTTEFGKSVI 120
 DB 61 kgllepaaifhlklpaindthcgligfnetacikkladgffefevlpkflttefgksvi 120
 OY 121 NYDVMEILTKTLGMDIOEELNLTGTHYSPKFDGCLGRLOGLKYYWVHFAFVLSM 180
 DB 121 nydvmeilctklgwdlgeelnltcthyppkfdrgligriglkyywvthasfvlasm 180
 OY 181 EKFAQAVRVLDSPDVPDVHDK 204
 DB 181 ekfaqavrvldslpdpvindhk 204

RESULT 3

ID AAW23944 standard; Protein; 204 AA.

XX AAW23944;

DT 30-JUN-1998 (first entry)

DE Human herpesvirus 8 Interleukin-6.

XX Interleukin-6; IL-6; human herpesvirus 8; HHV8; shotgun-cloning;
 KW antibody; diagnosis; treatment.
 XX Human herpesvirus 8.
 OS

PN WO9803657-A1.

PD 29-JAN-1998.

PF 19-JUL-1996; 96WO-EP03199.

PR 19-JUL-1996; 96WO-EP03199.

PA (BEHM) BEHRING DIAGNOSTICS GMBH.
 PA (UNIV) UNIV NEW YORK STATE.
 XX
 PI Albrecht J, Fleckenstein B, Friedman-Kien A, Huang Y;
 PI Neipel F;
 XX
 DR WPI; 1998-120781/11.
 XX
 PT Viral interleukin-6 produced recombinantly from human herpes virus 8
 PT DNA - and related nucleic acid and antibodies, used for diagnosis
 PT and treatment of herpes 8 infection or related diseases, e.g. Kaposi
 PT sarcoma
 XX
 PS Claim 2; Fig 2; 19pp; English.
 XX
 CC The interleukin-6 (IL-6) and protein AAW23945 derived from the sequence
 CC can be used to detect antibodies and antibodies can be used to detect
 CC IL-6. This can be used for the diagnosis of HHV8 infection or
 CC associated diseases such as Kaposi sarcoma or kidney cell carcinoma.
 CC Antibodies, proteins and the gene sequence can all be used in the
 CC treatment of infections and diseases as mentioned above.
 CC
 XX
 SO Sequence 204 AA;

Query Match 100.0%; Score 1095; DB 19; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.7e-118;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCFRKLMSLLVSLVSGTRGKLPAPFERKLLIQLNMLWLVDECFRDLCTRTGIC 60
 DB 1 mcfkrlmsllvsgtrgklpapefekdliqlnmlwlvdecfdrldcyrtygic 60
 QY 61 KGLLEPAALFHLKLPAINDTDHGCLIGFNETSCLKRLADGFEFEVLEFKLTTEFGKSVI 120
 DB 61 kgllepaalfhlklpaindthcgllgfnetsclkladgfevlfklttefgsvi 120
 QY 121 NVDVMEUFLTKTLGMDIQEELNKLTKTHYSPKFDRLGLGRLQGLKTYVHRFASFYVLSAM 180
 DB 121 nvdvmeufltktlgmdiqeelnlktkthyspkfdrgllgrlqglkyvhrfasyvlsam 180
 QY 181 EKFAQAVRVLDSTIPVTPVHDK 204
 DB 181 ektaqavrvldstipvtpvhnk 204

RESULT 4

AAW95015
 ID AAW95015 standard; peptide; 185 AA.
 XX

AC AAW95015;
 XX

DT 21-MAY-1999 (first entry)
 XX

DE Kaposi's sarcoma herpes virus interleukin-6 (IL-6) polypeptide.
 XX

KW Cytokine: interleukin-B30; IL-B30; forensic science; cell proliferation;
 XX inflammatory condition; drug screening; human; IL-6.
 XX

OS Kaposi's sarcoma herpes virus.
 XX

PN WO9905280-A1.
 XX

PD 04-FEB-1999.
 XX

PF 24-JUL-1998; 98WO-US15423.
 XX

PR 25-JUL-1997; 97US-0900905.
 XX

PA (SCHE) SCHERING CORP.
 XX

PI Hazan JF;
 XX

DR WPI; 1999-142935/12.
 XX
 XX Newly isolated or recombinant polynucleotide encoding mammalian
 PT cytokine interleukin-B30 (IL-B30). Including fragments - useful for
 PT regulating activation, development, differentiation and function of
 PT various cell types, and for diagnosing and treating conditions
 PT associated with IL-B30
 XX
 PS Disclosure; Page 11-12; 83pp; English.
 XX

CC This invention relates to mammalian cytokine interleukin-B30 (IL-B30)
 CC polypeptides. Host cells containing a vector comprising the IL-B30
 CC nucleic acids are used for the recombinant production of the proteins.
 CC The polynucleotides are useful for diagnosis of IL-B30 mediated
 CC conditions, and forensic science (e.g. to distinguish rodent from human,
 CC or as a marker to distinguish between different cells exhibiting
 CC differential expression or modification patterns). The IL-B30 (including
 CC fragments), together with antibodies that bind to IL-B30 are useful for
 CC teaching purposes. They are also used for treating conditions associated
 CC with abnormal physiology or development, including inflammatory
 CC conditions. The polypeptide cytokine should mediate cytokine synthesis
 CC and proliferation in cells. IL-B30 is useful for drug screening to
 CC identify compounds having binding affinity to IL-B30. The present
 CC sequence represents a Kaposi's sarcoma herpes virus IL-6.
 XX

SO Sequence 185 AA;

Query Match 90.6%; Score 992; DB 20; Length 185;
 Best Local Similarity 100.0%; Pred. No. 1.8e-106;
 Matches 185; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 TRGKLPAPFERKDLIIQRLNMLWLVDECFRDLCTRTGICKILPEALFHLKLPAIND 79
 DB 1 trgklpapefekdliiqlnmlwlvdecfdrldcyrtygikglepaalfhlklpaind 60
 QY 80 TDHCGCLGFNETSCLKRLADGFEFEVLEFKLTTEFGKSVINVDVMEUFLTKTLGMDIQEE 139
 DB 61 tdhcgclgfnetsclkladgfevlfklttefgksvinvdvmeufltktlgmdiqee 120
 QY 140 LNKLTHTHSPKFDRLGLGRLQGLKTYVHRFASFYVLSAMEFAGQAVRVLDSTIPVTP 199
 DB 121 lnkltkthyspkfdrgllgrlqglkyvhrfasyvlsamekfagqavrvldstipvtp 180
 QY 200 DVHDK 204
 DB 181 dvhdk 185

RESULT 5

AAW02611
 ID AAW02611 standard; protein; 184 AA.
 XX

AC AAW02611;
 XX

DT 24-FEB-1997 (first entry)
 XX

DE Interleukin-6 (F74Y, Q75F, S76L, Q175L, S176R, Q183A).
 XX

KW Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
 XX bovine; granulocyte colony stimulating factor; bc-CSF; receptor; gp130;
 KW thrombocytopoiesis; haematopoietic progenitor cell; rheumatoid arthritis;
 KW bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
 KW breast cancer; infectious disease; bone marrow progenitor cell; therapy;
 KW postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
 XX

OS Homo sapiens.
 XX

PN
 XX

PD
 XX

PF
 XX

PR
 XX

PA
 XX

PI
 XX

Location/Qualifiers

Key 74 /note= "F74Y"

Misc-difference 75 /note= "Q75F"

[illegible]

DR	WPI: 1996-300575/30.
XX	
PT	Identifying interleukin-6 super-agonists and (super)antagonists -
PT	using a 3-dimensional model of bovine granulocyte colony stimulating
PR	factor to identify binding sites
XX	
PS	Claim 10; ; 26pp: English.
CC	
CC	AAW08476-W08478 represent human interleukin-6 (IL-6) mutants (see
CC	AAW02609 for wild type sequence), with greater affinity for the receptor,
CC	which can be used as IL-6 antagonists and superantagonists. These
CC	sequences were identified using the method of the invention. The method
CC	comprises comparing IL-6 with the bovine granulocyte colony stimulating
CC	factor (bg-CSF) sequence. On the basis of this comparison a
CC	3-dimensional model of IL-6 is formulated, which allows the
CC	identification of residues that form the site of interaction with the
CC	specific receptor, and those that constitute the site of interaction with
CC	gp130. The method can be used to identify superagonists, antagonists,
CC	and superantagonists of IL-6. The IL-6 superagonists identified by this
CC	method can be used for the treatment of thrombocytopenia, and for the ex
CC	vivo expansion of human haematopoietic progenitor cells for bone marrow
CC	transplantation and gene therapy. They can also be used for the
CC	treatment of breast cancer, leukemia, and infectious diseases or
CC	diseases connected with disorders of bone marrow progenitor cells. The
CC	antagonists and superantagonists identified by the method can be used for
CC	the treatment of diseases characterised by the overproduction of IL-6,
CC	particularly multiple myeloma, rheumatoid arthritis, postmenopausal
CC	osteoporosis, and systemic lupus erythematosus. The method can also be
CC	used to identify IL-6 variants with a greater affinity for the specific
CC	receptor (see AAW02610-W02612), or variants with a reduced or abolished
CC	affinity for gp130.
SQ	
XX	Sequence 184 AA:
OY	
Query Match	16.9%; Score 185.5; DB 17; Length 184;
Best Local Similarity	28.0%; Pred. No. 2.2e-13;
Matches 44; Conservative 31; Mismatches 71; Indels 11; Gaps 1;	
OY	46 IDECRRL-----CYRTGICKGLPEPAIFHLKLPAINDTDHCGLGFNETSCL 94
Dd	: :- - - - - - - - - - - - - - - - 11111
Db	25 ldkqrlrdldfslarkctcnsmncsskkaeenlilpmakdcyflglnectl 84
OY	95 KLIADGFEEFLVLTTEFGSVINVDVMELTKTGMIDQELNKLTKTHSPPKFD 154
Dd	: : : : : :
OY	85 vkitlgillefeyleylgnrfessegegaraymrktqlgfkkaknldaiteptpcrn 144
OY	155 RGLLGRLOGLKRYWRHFAFSFYVLASMEKFAGAVAEYL 191
Dd	: :- - - - - - - - - - - - - - - - 11111
Db	145 asllklkgapnwqmdmtlhlllrfaekellrslral 181
RESULT 8	
ID	AAW08476 standard; Protein: 184 AA.
AC	AAW08476;
XX	
XX	24-FEB-1997 (first entry)
DE	Interleukin-6 variant #1.
XX	
KM	Interleukin-6; IL-6; human; superagonist; antagonist; superantagonist;
KM	bovine; granulocyte colony stimulating factor; bg-CSF; receptor; gp130;
KM	thrombocytopenia; haematopoietic progenitor cell; rheumatoid arthritis;
KM	bone marrow transplantation; gene therapy; multiple myeloma; leukaemia;
KM	breast cancer; infectious disease; bone marrow progenitor cell; therapy;
KM	postmenopausal osteoporosis; systemic lupus erythematosus; hormone.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FH	Misc-difference 31

```

FT      /note= "Y31D"
FT      Misc-difference 35
FT      /note= "G35F"
FT      Misc-difference 75
FT      /note= "Q75Y"
FT      Misc-difference 76
FT      /note= "S76I"
FT      Misc-difference 118
FT      /note= "S118R"
FT      Misc-difference 121
FT      /note= "V121D"
FT      Misc-difference 175
FT      /note= "Q175I"
FT      Misc-difference 176
FT      /note= "S176R"
FT      Misc-difference 183
FT      /note= "Q183A"
XX
XX      W09618648-A1.
XX
XX      20-JUN-1996.
XX
XX      13-DEC-1995; 95MO-1T00216.
XX      14-DEC-1994; 94IT-0RM0805.
XX
XX      (RICE-) 1ST RICECUE BIOL MOLECULAR ANGELETTI.
XX
XX      Ciliberto G, Lahm A, Savino R, Toniatti C;
XX
XX      WPI: 1996-300575/30.
XX
XX      Identifying Interleukin-6 super-agonists and (super)antagonists -
XX      using a 3-dimensional model of bovine granulocyte colony stimulating
XX      factor to identify binding sites
XX
XX      Claim 10; : 26pp; English.
XX
XX      AAM08476-W08478 represent human Interleukin-6 (IL-6) mutants (see
XX      AAM02609 for wild type sequence), with greater affinity for the receptor,
XX      which can be used as IL-6 antagonists and superantagonists. These
XX      sequences were identified using the method of the invention. The method
XX      comprises comparing IL-6 with the bovine granulocyte colony stimulating
XX      factor (bc-CSF) sequence. On the basis of this comparison a
XX      3-dimensional model of IL-6 is formulated, which allows the
XX      identification of residues that form the site of interaction with the
XX      specific receptor, and those that constitute the site of interaction with
XX      gp130. The method can be used to identify superagonists, antagonists,
XX      and superantagonists of IL-6. The IL-6 superagonists identified by this
XX      method can be used for the treatment of thrombocytopenia, and for the ex
XX      vivo expansion of human hematopoietic progenitor cells for bone marrow
XX      transplantation and gene therapy. They can also be used for the
XX      treatment of breast cancer, leukemia, and infectious diseases or
XX      diseases connected with disorders of bone marrow progenitor cells. The
XX      antagonists and superantagonists identified by the method can be used for
XX      the treatment of diseases characterised by the overproduction of IL-6,
XX      particularly multiple myeloma, rheumatoid arthritis, postmenopausal
XX      osteoporosis, and systemic lupus erythematosus. The method can also be
XX      used to identify IL-6 variants with a greater affinity for the specific
XX      receptor (see AAM02610-W026112), or variants with a reduced or abolished
XX      affinity for gp130.
XX
XX      Sequence 184 AA:
XX
XX      Query Match 16.8%; Score 184.5; DB 17; Length 184;
XX      Best Local Similarity 28.0%; Pred. No. 2.8e-13;
XX      Matches 44; Conservative 31; Mismatches 71; Indels 11; Gaps 1;
QY      46 IDECFRDL-----CYRTGICGKILPFAIFHLKLPAINDTDHGILGFNETSCL 94
Db      25 idkqjrdlildfalslrkctcnksmccsskaelaennlnlpmkaekdcgcyfgneetcl 84

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QY      95 KKLADGFEFEVLEFKLTTFEGKSVINVDVMEELTKTLGMDIOEELNKLTKTHYSPKRD 154
Db      85 klltqlllefyeyleylqnrffesseeqaravqmrckdlqfkkaknldaltlppdptn 144
QY      155 RGLLGRLOGLKRWVRHFAFSFYLSAMEKFAAGAVRL 191
Db      145 asllcklqgnqwidmtchlllrsfkelllrsal 181

RESULT 9
AAP81162
ID AAP81162 standard; protein; 201 AA.
XX
XX      AAP81162:
XX
XX      15-OCT-1990 (first entry)
XX
XX      Polypeptide with B-cell differentiation factor (BCDF) activity.
XX
XX      B-cell differentiation factor; BCDF; cancer; autoimmune.
XX
XX      Homo sapiens.
XX
XX      EP257406-A.
XX
XX      02-MAR-1988.
XX
XX      06-AUG-1988; 88EP-0111409.
XX
XX      06-AUG-1986; 86JP-0184858.
XX      27-AUG-1986; 86JP-0200433.
XX      18-DEC-1986; 86JP-0302699.
XX      13-MAY-1987; 87JP-0116332.
XX
XX      (AJIN) AJINOMOTO KK.
XX
XX      kishimoto TN, Hirano T, Matsui H, Takahara Y, Akiyama Y, Okano A;
XX
XX      WPI: 1988-057698/09.
XX
XX      Purified polypeptide with B-cell differentiation factor activity -
XX      useful in prodn. of antibodies for diagnosis and therapy of
XX      cancers, infectious diseases etc.
XX
XX      Claim 12; Page 41; 72pp; English.
XX
XX      Peptide with BODF activity may be used in the production and
XX      repeat of B-cells, it is useful in treatment of autoimmune
XX      diseases, malignant tumors and may be used to influence B-cells
XX      to produce Abs in vitro.
XX
XX      Sequence 201 AA:
XX
XX      Query Match 16.8%; Score 184; DB 9; Length 201;
XX      Best Local Similarity 28.1%; Pred. No. 3.6e-13;
XX      Matches 41; Conservative 31; Mismatches 74; Indels 0; Gaps 0;
QY      46 IDECFRDLCTYRTGICGKILPFAIFHLKLPAINDTDHGILGFNETSCLTKLADGFEFE 105
Db      53 idkirkctcnksmccsskaelaennlnlpmkaekdcgcyfgneetclvklqllle 112
QY      106 VLFKFLTTEFGKSVINVDVMEELTKTLGMDIOEELNKLTKTHYSPKRDGILGRLOGLK 165
Db      113 vyleylqnrffesseeqaravqmrckvllqfkkaknldaltlppdptnallcklqgn 172
QY      166 YWVRHFAFSFYLSAMEKFAAGAVRL 191
Db      173 qwidmtchlllrsfkelllrsal 198

RESULT 10
AAM07200

```


ID	AAW07200 standard; Protein; 184 AA.
AC	AAW07200;
DT	22-JUL-1997 (first entry)
DE	Human interleukin 6 antagonist Sant'7.
KW	Interleukin 6; IL-6; gp130; binding; hIL-6 DRD; treatment; multiple myeloma; rheumatoid arthritis; lupus erythematosus; osteoporosis.
OS	Synthetic.
FT	Key Location/Qualifiers
FT	Misc-difference 31 /note- "Asp substituted for wild type Tyr"
FT	Misc-difference 35 /note- "Phe substituted for wild type Gly"
FT	Misc-difference 57 /note- "Leu substituted for wild type Asp"
FT	Misc-difference 59 /note- "Glu substituted for wild type Phe"
FT	Misc-difference 60 /note- "Asn substituted for wild type Trp"
FT	Misc-difference 75 /note- "Gln substituted for wild type Tyr"
FT	Misc-difference 76 /note- "Ser substituted for wild type Lys"
FT	Misc-difference 118 /note- "Arg substituted for wild type Ser"
FT	Misc-difference 175 /note- "Gln substituted for wild type Ile"
FT	Misc-difference 176 /note- "Ser substituted for wild type Arg"
FT	Misc-difference 183 /note- "Gln substituted for wild type Ala"
PN	WC9634104-A1.
PD	31-OCT-1996.
XX	
PP	26-APR-1996; 96MO-IT00084.
PR	28-APR-1995; 95IT-ORW0273.
PA	(RICE-) IST RICERCH E BIOL MOLECOLARE ANGELETTI.
PI	Ciliberto G, Paonessa G, Savino R;
DR	WPI: 1996-497635/49.
N-PSDB:	AAT44359.
PT	New human Interleukin-6 antagonists - incapable of binding gp 130, used for treating e.g. multiple myeloma, arthritis or osteoporosis
Claim 1:	Page 21-22; 30pp; English.
CC	The present sequence is Sant'7, a human interleukin-6 (hIL-6) antagonist. Sant'7 and other hIL-6 antagonists (AAW07197-199) are characterised in that they are totally incapable of binding gp130. Mutations were introduced into four codons in the region coding for hIL-6 cloned into pT7.7/IL-6/pFRD/hind, creating the following amino acid substitutions: Y31D, G35F, S118R and V121D. These mutations drastically reduced the biological activity of the cytokine, without altering its ability to bind to the hIL-6 receptor, thus generating hIL-6 DRD (see AAW07201). Sant'7 was generated from Sant'5 (contg. 5 extra mutations: Q75I, S76K, Q175I, S176R and Q183A) by inserting 3 more amino acid substitutions: L157D, E59F and N60W. The hIL-6 antagonists can be used for the prepn. of pharmaceutical cpds. for the treatment of multiple myeloma, rheumatoid arthritis, lupus erythematosus and osteoporosis.
Sequence	184 AA:

```

Query Matched:          16.8%; Score 193.5; DB 17; Length 184;
Best Local Similarity   27.4%; Pred No. 3.7e-13;
Matches 43; Conservative 32; Mismatches 71; Indels 11; Gaps 1

QY      46 IDECFNDL-----CYRTGICKGILPEAIPFLKLPAINDTDHGLIGFNETSCL 94
           ||:|||||         |::||::|||::|||::|||::|||::|||::|||
Db       25 Idkgrfdldflsalrketcnkanmcscskadafwnlplmaekdcfygfneetcl 84
QY      95 KKLDAGFEFEEVLEFKFTTFEFGSVYNVDVMELTTLTGMDOBELNKLTIKHYSPRPFD 154
           ||::|||||::|||::|||::|||::|||::|||::|||::|||::|||
Db       85 vkltgtllefeyleyqlgnrtfessseqaravqnrctdlqgfiqqkaknldaaitcpdptn 144
QY      155 RGLGRLOGLGKYWWRHPSFYVLNAMESKFAGAVRYL 191
           ||:|||||::|||::|||::|||::|||::|||::|||::|||
Db       145 asltkigagngwlgdmthlllrstkeflrstal 181

RESULT_11
AAW58519
AAW58519 standard; protein; 184 AA.
XX
AC      AAW58519;
XX
DT      28-AUG-1998 (first entry)
XX
DE      Human Interleukin 6 mutant with superantagonist activity San7.
XX
KW      Human; Interleukin 6; IL-6; hIl-6; superantagonist; San7; San7;
KM      mutant; adenoviral vector; multiple myeloma; Castleman's disease;
MM      mesangial glomerulonephritis; osteoporosis; Rheumatoid arthritis.
XX
OS      Synthetic.
XX      Homo sapiens.
PN      W098I3383-A1.
PD      02-APR-1998.
XX
PF      24-SEP-1997; 97MO-IT00231.
XX
PR      24-SEP-1996; 96IT-RM00650.
XX
PA      (CNRS ) CNRS CENT NAT RECH SCI.
PA      (RICE-) IST RICERCHE BIOL MOLECOLARE ANGELETTI.
XX
PI      Caliberto G, Perricaudet M, Saggio I, Savino R;
DR      MPI; 1998-230636/20.
XX
PT      Recombinant defective adenovirus encoding antagonistic mutant of
PT      human Interleukin-6 - Is used to treat excessive production of this
PT      cytokine and to prolong expression of therapeutic protein from
PT      adenoviral gene therapy vectors
XX
PS      Claim 4; Page -: 19pp; English.
CC      New recombinant defective adenovirus vector have been developed which
CC      contain at least 1 DNA sequence encoding a mutant form of human
CC      interleukin-6 (hIL-6), or its fragment or derivative, that has
CC      antagonist or superantagonist activity against hIL-6. The present
CC      sequence represents a mutant hIL-6 with superantagonist activity having
CC      the mutations: Y31D, G35P, L57D, E59P, N60W, Q75Y, S76K, S118R, V121D,
CC      Q175I, S176R and Q183A designated San7. The DNA sequence is placed
CC      under control of elements that provide expression in selected cell
CC      types, particularly the Rous sarcoma virus promoter. The adenovirus
CC      vector can be used to treat and/or prevent conditions associated with
CC      overproduction of IL-6, specifically multiple myeloma, Castleman's
CC      disease, mesangial glomerulonephritis, osteoporosis, Epstein-Barr
CC      positive lymphoma, rheumatoid arthritis and systemic lupus erythematosus
CC      Cells and implants are used to express a gene encoding a therapeutic
CC      protein. The adenovirus vector can be administered by injection.
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SQ Sequence 500 AA;
 Query Match 16.8%; Score 183.5; DB 18; Length 500;
 Best Local Similarity 25.4%; Pred. No. 1.4e-12;
 Matches 48; Conservative 38; Mismatches 88; Indels 15; Gaps 2;
 OY 18 SGTGKLPDAP--EFKDL-----LIQRLNMLMWIDECFRDLCYRTGCKG 62
 Db 309 sgsgsgsvpevypgedskdvaaphrqphtsserldkqiryllgdlsalrketcnkmces 368
 OY 63 ILPPAIFHLKLPAINDTDHGGLIGFNETSCLKKLDGFEFEVLEFKLTTEFGKSYINV 122
 Db 369 skelaennlnlpkmaekdgcfsqfneetclvklitgllfeyleylqnrtesseega 428
 OY 123 DVNELLTKTLGWDIOEELNKLRTHTSPPKFDRLGRLGGLKYWVRHFAFVLSAMEK 182
 Db 429 ravqmsclkvllgflqkkaaknldaitpdpptnaslltklqagqvwldmtthlltsfke 408
 OY 183 FAGQAVRVL 191
 Db 489 flqsslrsl 497
 RESULT 14
 AAW36846
 ID AAW36846 standard; Protein; 525 AA.
 AC AAW36846;
 XX
 DT 25-MAR-1998 (first entry)
 XX
 DE Human fusion polypeptide H-IL-6 with 18 amino acid linker.
 XX
 KM Interleukin-6; IL-6; interleukin-6 receptor; IL-6R; ligand; conjugate;
 KW protein interaction; therapeutic; antagonist.
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= signal_peptide
 FT /note= "H-IL-6 fusion polypeptide"
 FT Region 324..341
 FT /label= linker region
 FT /note= "Links together COOH-terminus of sIL-6R with
 the NH2-terminus of IL-6"
 XX
 PN MO9732891-A2.
 XX
 PD 12-SEP-1997.
 XX
 PF 07-MAR-1997; 97MO-DE00458.
 XX
 PR 07-MAR-1996; 96DE-4008813.
 XX
 PA (ANGE-) ANGEWANDTE GENTECHNOLOGIE SYSTEME GMBH.
 PA Rose-John S;
 PI
 XX
 DR MPI: 1997-470536/43.
 DR N-PSDB; AAT97848.
 XX
 XX Conjugate of two peptide(s) with mutual affinity connected by a
 PT linker - used to modulate interactions between proteins, e.g. for ex
 vivo expansion of human stem cells
 XX
 PS Disclosure; Fig 1; 19pp; German.
 XX
 CC This sequence represents the fusion polypeptide H-IL-6 which contains
 CC an 18 amino acid linker which joins the carboxy terminus of human

CC Interleukin-6 receptor (IL-6R) with the amino terminus of human
 CC interleukin-6 (IL-6). Such conjugates could be used to modulate
 CC interactions between proteins, particularly to overcome interrupted
 CC interactions caused by an incomplete interleukin-6 (IL-6) receptor. These
 CC constructs derived from IL-6 and its receptor, can also be used for ex
 vivo expansion of human stem cells, and as a therapeutic IL-6 receptor
 CC antagonist.
 XX
 SQ Sequence 525 AA;
 Query Match 16.8%; Score 183.5; DB 18; Length 525;
 Best Local Similarity 25.4%; Pred. No. 1.5e-12;
 Matches 48; Conservative 38; Mismatches 88; Indels 15; Gaps 2;
 OY 18 SGTGKLPDAP--EFKDL-----LIQRLNMLMWIDECFRDLCYRTGCKG 62
 Db 334 sgsgsgsvpevypgedskdvaaphrqphtsserldkqiryllgdlsalrketcnkmces 393
 OY 63 ILPPAIFHLKLPAINDTDHGGLIGFNETSCLKKLDGFEFEVLEFKLTTEFGKSYINV 122
 Db 394 skelaennlnlpkmaekdgcfsqfneetclvklitgllfeyleylqnrtesseega 453
 OY 123 DVNELLTKTLGWDIOEELNKLRTHTSPPKFDRLGRLGGLKYWVRHFAFVLSAMEK 182
 Db 454 ravqmsclkvllgflqkkaaknldaitpdpptnaslltklqagqvwldmtthlltsfke 513
 OY 183 FAGQAVRVL 191
 Db 514 flqsslrsl 522
 RESULT 15
 AAR77387
 ID AAR77387 standard; Protein; 169 AA.
 AC AAR77387;
 XX
 DT 17-APR-1996 (first entry)
 XX
 DE Human IL-6 mutant IL-6a (amino acids 5-19 deleted).
 XX
 KM Human interleukin-6; IL-6a mutant; increased stability;
 KW recombinant; production; deletion mutant; amino acids 5-19.
 OS Homo sapiens.
 OS JP07224097-A.
 PN
 PD 22-AUG-1995.
 XX
 PF 08-FEB-1994; 94JP-0014461.
 XX
 PR 08-FEB-1994; 94JP-0014461.
 XX
 PA (ASAG) ASahi GLASS CO LTD.
 PA
 DR MPI: 1995-325556/42.
 DR N-PSDB; AAO94342.
 XX
 PT Interleukin-6 mutant, related DNA and expression vectors - has
 PT higher stability than natural interleukin-6
 XX
 PS Claim 1; Page 10; 18pp; Japanese.
 XX
 CC AA094342 encodes AAR77387 the human IL-6 deletion mutant IL-6a, which
 CC lacks the amino acids Gly5-Leu19 of the wild type protein. The
 CC cDNA can be used for the recombinant prodn. of IL-6a, which has
 CC increased stability compared to wild type IL-6.
 XX
 SQ Sequence 169 AA;

